Run on:

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RESULT 1
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-MODEL=frame+ p2n.model.-DEV=Xlp
-Q=/Capt2_1/USPTO_Spool_p/US09043944/runat_11122003_062400_3671/app_query.fasta_1.647
-Q=/Capt2_1/USPTO_Spool_p/US09043944/runat_11122003_062400_3671/app_query.fasta_1.647
-DB=GenEmb1 -QFWT=fastap -SUFPTX=rge -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -SCORE=C - THR MAX=100 -ALFR MIND=0 -ALIGHOUS - SOURCH=0-COTPWT=pto -NORM=ext -HEAPEISTES=500 -MINEDN=0 -MAXLEN=200000000
-USER=US09043944 @CGN 1 1 4958 @runat_11122003 062400_3671 -NCPU=6 -ICPU=3
-NO MANAP -LARGEOGUERY -NGG SCORES=0 -WAIT -DSPEDCACE-100 -LONGLOG
-FGAPORT=12 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                     December 11, 2003, 06:24:06; Search time 4227 Seconds (without alignments) 4461.637 Million cell updates/sec
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1 MPSTRRQQEGGGADAETHTV.......YYINSLFLPFLCIINFSIIS 461
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                    OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                     7.0
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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Maximum DB seq length: 2000000000
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Perfect score:
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                         em htg mus: em htg pln: *
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em htg vrt: *
      em_htg_hum:*
38:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	5660 Caenorhal	64 Ca	1540 Caellot Habot 043492 Gallus G	1936 Bos taur	5330	5621 Sequenc	1146 Sequenc	48 Sequenc	L42110 Homo sapien	Secretary Secretary	7309 Sequenc	96 Sequenc	5768 Sequenc		53	U78084 Drosophila		edneuc	AK134366 Sequence	Segrenc	lomo sapi	Sequenc	7181 Sequenc	1368 S	თ თ	o c	ARUBOLESS SEQUENCE	7 Sequenc	9	Šē	Σ	snw snw 601	A63557 Sequence 10	9	4 Drosophil	7024 Drosoph	20183 Seguenc	37338 Sequenc	34525 Sequenc	26797 Seguenc	
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                                                                             ATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATATAGTCAAAACAATGGAAGG
                                                              WetAlaLeuValValPheThrMetAsnThrIleThrPheTyrSerGlnAsnAsnGlyArg
                                                                                                                    HisLeuLeuSerHisProPheValArgGluThrAspSerIleValGluLysGlyLeuMet
                                                                                                                                                                               SerbeuglyAsnAlaLeuValMetLeuCysValValValLeuMetThrValLeuLeuIle
                                                                                                                                                                                                                                  ValPheTyrLysPyrLysPheTyrLysLeuIleHisGlyTrpLeuIleValSerPhe
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IGLCFILVLLAVFKRALPALQFFFSPDSFFFFVPAGSSPHLLHKSLKSVYXINSLFLP
                 mRNA linear INV 23-JAN-1996 protein (sel-12) mRNA, complete
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                                                                                                                                                                                                                                                                                                        Columbia
                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (07-SEP-1995) Diane Levitan, Biochemistry, Colu
University, 630 W 168th St., New York, NY 10032, USA
On Dec 9, 1995 this sequence version replaced gi:1000566.
Location/Qualifiers
                                                                                               Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis
                                                                                                                                                        l (bases 1 to 1461)
Levitan, D. and Greenwald, I.
Facilitation of lin-12-mediated signalling by sel-12,
Caenorhabditis elegans S182 Alzheimer's disease gene
96032531
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Matches:
Conservative:
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Caenorhabditis elegans membrane
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Best Local Similarity:
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U35660.1
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Percent Similarity: 99.33% Conservative: 0 Best Local Similarity: 99.33% Mismatches: 2 Query Match: 95.16% Indels: 1 DB: 3 Gaps: 0 US-09-043-944-1 (1-461) x AP171064 (1-1335)	Oy 1 MetProSerThrArgArgGlnGlnGlnGlyGlyGlyAlaAspAlaGluThrHisThrVal 20	OY 21 TYTGIYTHTASTLEUTHETHTASTARGASTSETGINGLUASFGLUASTVALVALGIUG 40	41 AlaGluLeuLysTyrGlyAlaSerHisVall1	Qy 61 MetalaLeuValValPheThrMetasnThrIleThrPheTyrSerGlnAsnAsnGlyArg 80	Qy 81 HisteuLeuSerHisProPheValArgGluThrAspSerIleValGluLysGlyLeuWet 100	Qy 101 SerLeuGlyAsnAlaLeuValMetLeuCysValValValLeuMetThrValLeuLeuIle 120 Db 301 TCACTTGGAAATGCTCGTCGTGTGTGTGGTGGTCGTTCTGATGACAGTTCTGCTGATT	OY 121 ValPheTyrLysTyrLysPheTyrLysLeulleHisGlyTrpLeulleValSerSerPhe 140	Oy 141 LeuLeuPheLeuPheTheThrThrIleTyrValGlnGluValLeuLysSerPheAspVal 160	Oy 161 SerProSerAlaLeuLeuValLeuPheGlyLeuGlyAsnTyrGlyValLeuGlyMetMet 180	Qy 181 CysIleHisTrpLysGlyProLeudrgLeuGlnGlnPheTyrLeuIleThrMetSerAla 200	Qy 201 LeumetAlaLeuValPhelleLysTyrLeuProGluTrpThrValTrpPheValLeuPhe 220	ArgTyrleu 2 AGATATTTG 7	Oy 241 ValgluThralagingiuArgAsnGluBrollePheProAlaLeuIleTyrSerSerGly 260	Qy 261 ValileTyrProTyrValLeuValThrAlaValGluAsnThrThrAspProArgGluPro 280	Qy 281 ThrSerSerAspSerAsnThrSerThrAlaPheProGlyGluAlaSerCysSerSerGlu 300	Qy 301 ThrProLysArgProLysValLysArgIleProGlnLysValGlnIleGluSerAsnThr 320 Db 901 ACGCCAAAAACGCCCAAAAACGCCAAAAACGCAAAAACGCAAAAACGCAAAAAA	321 ThralaSerThrThrGlnAenSerGlyValArgValGluArgGluleuAlaAlaGluArg 34
	Oy 441 ValTyrTyrIleAsnSerLeuPheLeuProPheLeuCysIleIleAsnPheSerIleIle 460 1321 GTTATTATATTATTATTATTATTATTATTATTATTATTAT	Qy 461 Ser 461 	RESULT 2 AF171064 LOCUS AF171064 LOCUS AF171064 DEFINITION Caenorhabditis elegans presenilin SEL-12 (sel-12) mRNA, complete	ACCESSION CAS. VERSION AF171064.1 GI:5759132 KEYWORDS .	SM	lph, c			25, Munich 81377, Germany Location/Qualifiers To a li 1335	/mol_type="mRNA" /mol_type="mRNA" /strain="N2" /db_xref="taxonn.6239" /chromosome="x"	gene 11335	/gune="ser.ls" /gune="ser.ls" /function="facilitator of Notch receptors signaling" /note="membrane protein; similar to Homo sapiens PS1 and PS2; similar to SE112 deposited in GenBank Accession Number AAA85511"	/codon_start=1 /product="presentlin_SEL-12" /protein_id="#AAD50991.1" /db_xref="d1:5759131.1"	/translation="MPSTRRQQEGGGDAETHTVYGTNLITNRNSQEDENVVEEABLK VGASHVTHLFVPPVSLCMALVVFTMNTITFYSONNGRHLLYTPPVRETDSIVERGLMSL GNALVMLCVVVLMTVLLIVFYKYKYKFYKLIHGWLIVSSFLLLFLFTTTIVYQEVLKSFDV SPSALVJLEGGRYĞVLGAMĞCTHWKGPLRLOOFYLITMSALMALVFFKYLEMVWEV	LFVISVMDLVAVLTPKGPLRYLVETAQERNEPIFPALIYSSGVIYPYJLYJAVENTTO PREPTSSDSNITSTFPERSSCSETPKRPKURKI PQRVQIESNTTASTTQNSGVRVER ELAAERPTVQDANFHRHEBERGVKLGLGDFFFFYSVLLGLGFRASSYFDMYTIASYVAIL IGLCFTLVLLAVPKRALPELPISFSGFIFYSVLLGLGFRASSYFDMYTIASYVAIL	345	Alignment Scores: Pred. No.: 1.11e-190 Length: 1335 Score: 2263.00 Matches: 442

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Coding segences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://worfdb.dfci.narvard.edu/), similarity to orber proteins from Blastx analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent. 's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers: tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids Res., 25, 955-964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.wormbase.org/db/seq/sequence?name=F35H12;class=Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TICE: This sequence may not be the entire insert of this clone. may be shorter because we only sequence overlapping sections:e, or longer because we provide a small overlap between
Direct Submission
Submitted (19-NOV-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
                                                                                                                                                      submitted (19-APR-2003) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                 Submitted (31-MAY-2003) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Sequencing Center
Department of Genetics, Washington University
L. Louis, MO 63110, USA, and
Sanger Centre, Hinkton Hall
Cambridge CB10 IRQ, England
email: submissions@watson.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The 5' cosmid is ZC13, 200 bp overlap; the 3' cosmid is F53H8, bp overlap. Actual start of this cosmid is at base position 1 o F35H12; actual end is at 12696 of F53H8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For a graphical representation of this cosmid sequence and its analysis see:
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Organism="Caenorhabditis elegans"
/mol_type="genomic DNA"
/strain="Bristol N2"
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gene="F35H12.6"
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Wilson, R.
                                                                                               8 (bases 1 to 27102)
Waterston, R.
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Waterston, R.
                                                 1081 GGTCTGGGCGACTTCATTTTTACTCTGTTCTCCTCGGCAAGGCTTCATCGTACTTTGAC 1140
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       1141 IGGAACACGACTATCGCCTGTTATGTGGCCATTCTTATGGTCTCTGCTTCACTCTTGTC 1200
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7 (Dases 1 to 27102)
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                                                                                                                                                                                                                                                TrpAsnThrThrIleAlaCysTyrValAlaIleLeuIleGlyLeuCysPheThrLeuVal
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Submitted (16-NOV-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
5 (bases 1 to 27102)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U41540 27102 bp DNA linear INV Caenorhabditis elegans cosmid F35H12, complete sequence.
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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Nelson, J. and Gattung, S.
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Waterston, R.
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yk400e8.3, yk400e8.5, yk452D8.3, yk452D9.5, yk490e8.3,
yk573H6.3, yk600e8.2,3, yk674e3.3, AF171064, U35660,
OSTF019E1.1, OSTR019E11.1"
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GNALWMLCVVVLMTVLLIVFYKYKFYKLIHGMLIVSSFILLELEFTIYVQEVLEKSFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPSALLVLFGLGNYGVLGMMCIHWKGPLRLQOFYLITMSALMALVFIKYLPEMTVWFV
LFVISVWDLVAVLTPKGPLRYLVETAQERNEPIFPALIYSSGVIYPYVLVTAVENTTD
PREPTSSDSNTSTAFPGEASCSSETPKRPKVKRIPQKVQIESNTTASTTQNSGVRVER
ELAAERPTVQDANFHRHEEEERGVKLGLGDFIFYSVLLGKASSYFDMNTTIACYVAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / translation="MRSSRHILSNVRPTIKNLDLTRGFSDRKTKYFDLNDLIKTVNVY
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YFYNNLIGLRVGHGKYNAAAAILDMQTFAFDEQKLSIDDLRAKFGIRAFYGYGSKDFLI
DEHQSEEVAMYFRSEEDHYVISNKQDAEKAIKEARKSFTTGKQFVTANFKEEGHFLQKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="MKSFFEQKKIRLICTNYPGSEFVTGGLHNSYTNQDRNSYMKSLM
ETLELKNVNRLIIMGHSRGGENALQLTSMNDENWPLVGAVMINSPGFAPHKGISKRMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="contains similarity to Interpro domains IPR000734 (Lipsse), IPR000379 (Esterase/lipsse/thioesterase, active site); coded for by the following C. elegans cDNAs: OSTR212H6 1, OSTR212H6 1.
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    ω
/note="contains similarity to Homo sapiens Glycophorin precursor Glycophorin E precursor; ENSEMBL:ENSP00000305872; coded for by the following C.
                                          following C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGLCFTLVLLAVFKRALPALPISIFSGLIFYFCTRWIITPFVTQVSQKCLLY"
                                                                                                                                                                                                                                                                       .5838,5884. .6203,
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join(7533. .7580,7730. .7867,7922. .8227,8270. .8349,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YPEFIVEVVDSIFDADKEVDTKI"
join(8003. .8220,8269. .8349,8659. .8744,8792. .9207)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="Suppressor/enhancer of lin-12 protein 12"
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                                             by the
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db_xref="WormBase:F35H12.5a"
                                                                                              /product="Hypothetical protein F35H12.6"
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                                                                                                                                                                                                                                                            join(5010, .5063,5134, .5324,5629, .
6265, .6348,6398, .6604,7027, .7295)
/gene="sel-12"
                                    legans cDNAs: yk1092f08.3"
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TINFIISLIKRHNKTINSILHPILHYFYNNLIGLRVSHGKVAAAAILPMOTFAFDEOK
LSIDDLRAKPGIRAFYGYGSKDFLIDEHQSEEVAMYFSEEDHYVISNKQDAEKAIKEA
RKSFTTGKQFVTANFKEEGHFLQKTYPEFIVEVVDSIFDADKEVDTKI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAAAATAATTTTTGGTCAGTGCATTGGTATTATGGTCAGTGCATTTGCAAGTCTGAGCT 5489
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                                                                                                                complement (join (9443. .9627,10392. .10517,10573. .10772, 10828. .11054,11147. .11335,11383. .11511,11615. .11845, 11895. .12010,12526. .12728,12776. .12893,12941. .13031))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 lulysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysValValValLeuMetT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 ----ThrValTyrGlyThrAsnLeuIleThrAsnArgAsnSerGlnGluAspGluAsnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 lyalglugluhladluheulysTyrGlyAlaSerHisValIleHisLeuPheValProVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 lSerbeuCysMetAlaLeuValValPheThrMetAsnThrIleThrPheTyrSerGlnAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5250 GTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGGTTTTATAGTCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5070 TATITAGACATITITATTITICTCAAGAACTAAAITGITAAAATTGCTACAAIGCALIGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5130 TCAGACCGTTTACGGTACAAATCTGATAACAAATCGGAATAGCCAAGAAGACGAAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5370 TTATCAATTTGCATCTGTGCAATCGCACTCTTTGTCAGTGCAAAATAATTTTTGGTCAGT
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                                                                                                                                                                                                                                                                                                                                322
                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                    complement (9443. .13031)
/gene="F35H12.4"
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AHLPOFOHGOMTENFPDNHLSNTNDNSERRRHDNSERRR VDQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIK ETDTIGQRALINSILINAAHTSVI VWTILLVVLYKYRCY YTLGEVFKTYNVAMDY TVALII IWNFGVVGMI CIHWKG FIKXLPEWTWLILAVISYDLVAALCPKGPLRMIVETA LVMMAEEDPEGQRKASKNSTYDKQAPANQSGNEDAEADD STPESRAAVQALPSNSQTSEDPEERGVKLGLGDFIFYSV 1.eGlyLeuCysPheThrLeuValLeuLeuAl 403 GlnPheProPheSerProAspSerPhePheT 423 SteuleutisLysSerLeuLysSerValTyrT 443 p mRNA linear VRT 02-SEP-2001 A, complete cds. CAAGCTTGCCACTTGCGCTAGTCACGAAAA 6928 ATTTTTTTAACAATAATTTTTTCATCTCTTC 6988 Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; protein; putative gamma-secretase; LCYSILEILEASNPheSerIleIleSer 461 rics, Children's Hospital of sburgh, 3460 Fifth Avenue, Lovelock, J. and Corey, S.J. Lovelock, J. and Corey, S.J. lus"

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora; Bovoidea, Bovidae, Bovidae, Bovinae, Bos.

E 1 (bases 1 to 1896)
S Sahara,N., Shirasawa,T. and Mori,H.
Molecular cloning of bovine presenilin 1 gene
L Unpublished
Onbellar (bonission
Sahara,N., Shirasawa,T. and Mori,H.
Direct Submission
L Whole (16-DEC-1997) Molecular Biology, Tokyo Institute of Psychiatry, 2-1-8 Kami-Kitazawa, Setagaya-ku, Tokyo 156, Japan
Location/Qualifiers
                                                                                                                                                                                                                                     1273
                                                                                                                                                                                                                                                                                                                                                       1393
     1028 ACTTACGATAAACAAGCTCCGGCAAACCAGTCTCAGAATGAAGATGCTGAAGCAGATGAT 1087
                                                                                                                   1139 ---ATTGAATCA----------ACACCTGAATCACGAGCTGCTGTTCAG--- 1174
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                                                                                                                                                  354
                                                                                                                                                                                                                                                                 AlaSerSerTyrPhe-----AspTrpAsnThrThrIleAlaCysTyrValAlaIleLeu 392
                                                                                                                                                                                                                                                                                                                                                                               -GlnPheProPheSerProAspSerPhePheThrPheValProAlaGlySerSerProHi 432
                                                                                                                                                                                                       GluArgGlyValLysLeuGlyLeuGlyAspPhellePheTyrSerValLeuLeuGlyLys
                                                                                                                                                                                                                               1214 GAAAGAGGAGTAAAGCTAGGTTTAGGAGACTTCATTTTCTACAGCGTCCTGGTTGGCAAA
                                                                                                                                                                                                                                                                                315 GlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArgValGluArg
                                                                                                                                                 335 GluLeuAlaAlaGluArgProThrValGlnAspAlaAsnPheHisArgHisGluGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                        sLeuLeuHisLysSerLeuLysSerValTyrTleAsnSer---LeuPheLeuProPh
                                295 AlaSerCysSerSerGluThrProLygArgProLygValLygArglleProGlnLysVal
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                                                           .088 GGNGGCTTTAGTCAAGAGTGGCAGCAACAAAGAGACAATAGAATAGGACCC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="brain"
9. 1445
/note="causal gene for familial Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eLeuCysIlelleAsnPhe 457
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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LVGKASATASCDWNTTLACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVFYFAT
DNLVQPFWDQLAFHQFYI"
389 c 406 g 529 t 10 otherb
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TTGTGCCTTACATTATTGCTCCTCGCCATTTTCAAGAAAGCATTACCAGCTCTTCCAG-- 1350
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ProGlyGluAlaSerCysSerSerGluThrProLysArgProLysValLysArgllePro
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GCAACAGCCAGTGGAGACTGGAACACAACCATTGCCTGTTTTGTAGCCATATTAATTGGT
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Potter, H. and Li, J.
Assay for identifying agents that inhibit non-disjunction
Patent: US 5985564-A 3 16-NOV-1999;
Location/Qualifiers
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YCYTAMLIVSSLLLEFESFIYLGEVEKTYNVAMDYISVALLIWNFGVVGMAAIHWKG
PLRLQQAYLLIWISALMALLYPIKYLPEWTAMLILAVISVYDLVAVLCPKGPLEMLVETA
QERNETLEPALIYSSTWWULVMNAEGDPEAQRKVSKNSNYNAQRPANSPVTTGTESE
SQDPVTESDDGGFSEEWEAQRDSRLGPHHSTAESRSAVQDLSSSILASEDPEERGVKI
GLGDFIFYSVLVGKASATASGDWNTTTACFVAILIGLCLTLLLAIFKKALPALPVSI
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                                                                                                  975 GAATGGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTG 1034
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                                                                                                                                                                                                                               PheProAlaLeuIleTyrSerStJyVallleTyrProTyrValLeuValThrAlaVal 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 GlnLysValGlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ArgGluLeuAlaAlaGlu 339
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                    915 CAGGCATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTTTATCAAGTACCTCCT 974
                                                                                                                                                          232 ThrProLysGlyProLeuArgTyrLeuValGluThrAlaGlnGluArgAsnGluProlle 251
                                                                                                                                                                                                                                                                                                                                                                                                292 ProGlyGluAlaSerCysSerSerGluThrProLysArgProLysValLysArgIlePro 311
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                           GluTrpThrValTrpPheValLeuPheValIleSerValTrpAspLeuValAlaValLeu
                                                                                                                                                                                                                                                                                                                  272 GluasnThrThrAspProArgGluProThrSerSerAspSerAsnThrSerThrAlaPhe
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Hale,R.S., Rowley,A.G. and Blackstock,W.G.
Novel assay
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GLAXO GROUP LIMITED (GB)
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                                                                                                       7596406
On Jul 25, 1995 this sequence version replaced gi:897613.
Original source text: Homo sapiens (clone: cc33) fetus brain cDNA
to mRNA.
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| note="map location near D14877, D148277, and D148268"
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216
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104
48
Rommens, J.M. and St. George-Hyslop, P.H. Cloning of a gene bearing missense mutations familial Alzheimer's disease.
Nature 375 (6534), 754-760 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 id="AAB46416.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-043-944-1 (1-461) x HUMS182R (1-2765)
                                                                                                                                                                                                                                                                                                                               'tissue_type="brain"
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/gene="S182"
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1 (Bases I to 2765)

1 (Bases I to 2765)

1 (Bases I to 2765)

1 Kedes, M. Chi, H., Lin, C., Li, G., Holman, K., Tsuda, T., Mar, L., Foncin, J.-F., Bruni, A.C., Montesi, M. P., Sorbi, S., Rainero, I., Pinnessi, L., Chumakov, I., Pollen, D., Brookes, A., Sanseau, P., Polinsky, R.J., Wasco, W., Da Silva, H.A.R., Haines, J.L., Pericak-Vance, M.A., Tanzi, R.E., Roses, A.D., Fraser, P.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGACCAATTAGCATTCCATCAATTTATATATCTAGCATATTTGCGGTTAGAATCCCATG 1676
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                                                                                                                                                                                                                                                                                                                                                  ------AAGTATAATGCAGAAAGCACAGAAAGG------1214
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      rgrccgaaaggrccacrrcgrargcrggrrgaaacagcrcaggaagaaargaaacgcrr 1094
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                                                                                                                                                                                                                                GluAsnThrAspProArgGluProThrSerSerAspSerAsnThrSerThrAlaPhe 291
                                                                                                                                                                                                                                                                                                              292 ProGlyGluAlaSerCysSerSerGluThrProLysArgProLysValLysArgIlePro 311
                                                                                                                                                                                                                                                                                                                                                                                          312 GlnLysValGlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg 331
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                                                                   ThrProLysGlyProLeuArgTyrLeuValGluThrAlaGlnGluArgAsnGluProIle 251
                                                                                                                                                 PheProAlaLeulleTyrSerSerGlyVallleTyrProTyrValLeuValThrAlaVal 271
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Homo sapiens (clone cc33) S182 m
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AUTHORS
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STS 15-JUN-1996
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-- Washington University/Merck EST sequence.
Location/Qualifiers
1. .2765
/organism="Homo sapiens"
                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 degrees C for 15 seconds 62 degrees C for 23 seconds 72 degrees C for 30 seconds 30 Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                          Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 others
                                                                               linear
                                                                                                                                G27112.1 GI:1375362
STS, STS sequence; primer; sequence tagged site.
Homo sapiens (human)
Homo sapiens
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                                                                                               human STS SHGC-31609, sequence tagged site.
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="taxon:9606"
/map="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer A: CTAACAAAGTCAAGATTCCCGG
Primer B: CAACTTCCGGGCCTATCATA
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50 mM
20 mM
                                                                                                                                                                                                                                                                                                                                                                                                                Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-043-944-1 (1-461) x G27112 (1-2765)
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                                                                                                                                                                                                                                                                                                           Contact: Richard M. Myers
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Total Vol:
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Polymerization:
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1677 GATGTTTCTTCTT 1689
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                                                                                                                                                                                                                                                                                                                                                                            Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MgC12:
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Best Local Similarity:
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JOURNAL
                                               RESULT 11
                                                                                                                                                                                                                                       REFERENCE
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                  132 HisGlyTrpLeuIleValSerSerPheLeuLeuPeuPheLeuPheThrThrIleTyrVal 151
                                                                                  GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171
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St. George-Hyslop, P. H., Rommens, J.M.
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St. George-Hyslop, P.H., Rommens, J.M. and Fraser, P.E. Genetic sequences and proteins related to alzheimer' Patent: 18 5986154-A 133 16-NOV-1999;
Location/Qualifiers
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1440 GCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCATATTAATTGGT 1499
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                        TGGAATTTTGGTGTGGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAG
                                                                                                      GlnPheTyrLeuIleThrMetSerAlaLeuMetAlaLeuValPheIleLysTyrLeuPro
                                                                                                                     CAGGCATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCT
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           GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu
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975 GAATIGGACTIGCGTGATCTTGGCTGTGATTTCAGTATATGATTATAGTGGCTGTTTTG 1034
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                                                                                      GAGACTGTGGGCCAGAGGCCCTGCACTCAATTCTGAATGCTGCCATCATGATGTGTC
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                        GlnGluAspGluAsnValValGluGluAlaGluLeuLysTyrGlyAlaSerHisValIle
                                                                                                                                                                         AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal
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                                                                                                 GlnLysValGlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg 331
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St. George-Hyslop, P.H., Rommens, J.M. and Fraser, P.E.
Methods for determining risk of developing alzheimer's disease l
detecting mutations in the presentilin 1 (PS-1) gene
Patent: US 6194153-A 133 27-FEB-2001;
Location/Qualifiers
                                                                                                                                                                                                                   GlyValLysLeuGlyLeuGlyAspPheIlePheTyrSerValLeuLeuGlyLysAlaSer
                                                                                                                                                                                                                                                                                                    SerTyrPhe-----AspTrpAsnThrThrIleAlaCysTyrValAlaIleLeuIleGly
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 uAsnThrThrAspProArgGluProThrSerSerAspSerAsnThrSerThrAlaPhe
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GCAACAGCCAGTGGAACTGGAACACAAACCTTACCTTTTCGTAGCCATATTAATTGGT
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HisGlyTrpLeulleValSerSerPheLeuLeuLeuPheLeuPheThrThrIleTyrVal	1260 GAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATACACCCTAGATCA 1319 340 ArgProThrValGlnAspalaAsnPheHisArgHisGluGluGluGluArg 356 1320 GGGCTGCTGTCCAGGAACTTTCCAGCAGTATCCTGGCTGG
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Db 1380 GGAGTADAACTTGGATTGGGAGATTTCTACAGTTGGTGGTGAAAGCCTCA 1439 Qy 377 SerTyrPheAppTracharthrth1leAlaCysTyvalAlalleLeul161y 394 :::::::::::::::::::::::::::::::::::	### Alignment Scores: Pred. No.: Score

us-09-043-944-1.rst

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: December 11, 2003, 06:24:06 ; Search time 2279 Seconds
(without alignments)
4916.351 Million cell updates/sec

Title:

US-09-043-944-1

Perfect score: 2378
Sequence:

I MPSTRRQQEGGGADAETHTV......YYINSLFLPFLCIINFSIIS 461

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 7.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 segs, 12152238056 residues
Total number of hits satisfying chosen parameters: 4556

45562784

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Listing first 45 summaries

Command line parameters:
-WODEL=frame+ p2n.model -DEV=xlp
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all larval stages, embryos, adults and dauers and the
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cDNAs were cloned into pPC8s"
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[Rabolidae, Peloderinae, Caenorhabditis.]

[Rabolidae, Peloderinae, Caenorhabditis.]

[Rabolidae, Vagilo, P., Rual, J. F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, C.M., Harley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Braces, J., Snyder, M., Hang, R., Chance, M.R., Lee, H., Tolias, P.P., Pecck, J., Snyder, M., Hang, R., Chance, M.R., Lee, H., Tolias, P.P., Checkte-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORPeanew version 1.1: experimental verification of the genome-annotation and resource for proteome-scale protein
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Jana Farber Canoer Institute
1 Jinmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Tel: 617 632 5739
Exa: 617 632 5739
Email: Marc Vidal@dci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
                                                                                                                                 423 ACAATCTATGTGCAAGAAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTT
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C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david_hill@dfci.harvard.edu or
marc vidal@dfci.harvard.edu
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
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Contact: Vidal M
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all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
a 118 c 149 g 138 t
Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
Sequence to predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115,
151: 617 632 5180
Fax: 617 632 5739
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditiodea;
Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 477)
Reboul,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T.,
Jackson,C., Shin-i,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,
Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
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all larval stages, embryos, adults and dauers and the
374 GGAGTAAGGGTGGAACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTT 315
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Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
17e1: 617 632 5180
Fax: 617 632 2425
Email: Jerome_Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans Ol philippe_vaglio@dfci.harvard.edu
Philippe_vaglio@dfci.harvard.edu
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1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA Tel: 617 612 5180
Fax: 617 612 5739
Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project: Contact david_hill@dfci.harvard.edu or
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[Rabditidae; Peloderinae; Caenorhabditis.]

[Rabditidae; Peloderinae; Caenorhabditis.]

[Reboul, J., Vaglio, P., Rual, J. P., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J. R., Hartley, J. L., Brasch, M. A., Vandenhaute, J., Boulton, S., Pracek, J., Jenna, S., Chevet, E., Papascotiropoulos, V., Tolias, P. P., Percek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Couctte-Stamm, L., Hill, D.E. and Vidal, M. C. elegans Orkeome version 1.1: experimental verification of the general annotation and resource for proteome-scale protein
                                                                               CB395382 494 bp mRNA linear EST 15-MAY-2003
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AGENCOURT_14365780 NIH_MGC_179 Homo sapiens cDNA clone
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 884)

subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

CDNAS were 2009 d 150 t
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Office of Cancer Genomics
National Cancer Institute / NIH
Bigg. 31 RulloMo7 Bethesda, MD 20892
Biggil: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
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/mol_type="mRNA"

/mol_type="mRNA"

/db_txef="taxon:9606"

/clone="type="pituitary"

/tissue_type="pituitary"

/lab_host="bituitary"

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/lab_host="miH MGC_179"

/clone=lorgan: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV

/clone="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV

/destroyed); Site 2: Not1; Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon cloning

). Average insert size 1.1 kb. Library was constructed by

(Invirogen). Note: this is a NIH_MGC Library."
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785 GTGGTTATGACCATCTTCCTTGGTGGTGCTCTACAAGTACCGTTGCTACAAGTTCATCCA
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDAM473 row: e column: 02
High quality sequence stop: 652.
Location/Qualifiers
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Mismatches:
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734.50
64.92%
53.77%
30.89%
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Best Local Similarity:
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AKU14706

Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833416A15 product:presenilin 2, full insert sequence.
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                                                                                                               340 CTGATGCTGCTGCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGACCTACAAT 399
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Rođentia, Sciurognathi, Muridae, Murinae, Mus.
            120 IlevalPheTyrLysTyrLysPheTyrLysLeuIleHisGlyTrpLeuIleValSerSer
                                                                                                                                                                      ValSerProSerAlaLeuLeuValLeuPheGlyLeuGlyAsnTyrGlyValLeuGlyMet
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
Mus musculus (house mouse)
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Mammalia; Eutheria;
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/lab_host="DH10B"
/clone lib="NHH MGC l24"
/roto="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
(destroyed); Site_2: Not1; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."
5 a 313 c 317 g 256 t
                       1101 bp mRNA linear EST 20-FEB-2002
_6531717 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732941
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                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1101)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12735 row: n column: 14
High quality sequence start: 9
High quality sequence stop: 643.
Location/Qualifiers
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103 TGCATGATCGTGGTGGTAGCCACCATCAGTCTGTGCGCTTCTCTACACAGAGAAGAATGGA
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5732941"
                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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                                                                                                                                             Homo sapiens (human)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

E (bases I to 1998)

Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Hara, A., Hayatsı, N., Hiramoto, K., Huroka, T., Hara, M., Hayatsı, N., Hiramoto, K., Huroka, T., Kato, H., Kato, H., Kato, H., Kato, H., Kato, H., Kato, H., Kato, H., Kato, H., Kato, H., Kayası, K., Sinii, Y., Konno, H., Kouda, M., Kasukawa, T., Kato, H., Kato, H., Kayası, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Oho, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Saito, R., Sakai, C., Sakai, K., Sanizaki, T., Sagaki, D., Shitaki, T., Tagami, M., Tagawa, A., Takahsahi, F., Tanaka, T., Tagami, M., Tagawa, A., Takahsahi, F., Tanaka, T., Tajama, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Shinaka, J., Direct Submission Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, I.-7.22 Suehiro-cho, Tsurumi-ku, Yokohama, Then, Menna and Mayashi E-mail: Genome research Group, Ranagawa 230-0045, Japan (E-mail: Genome research Group, Ten., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, M., Maranaka, Maranaka, M., Maranaka, M., Maranaka, Maranaka, Maranaka, Maranaka, Maranaka, Maranaka, Maranaka, Maranaka, Maranaka, Maranaka, Maranaka, Maranaka, Maranaka, Maranaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAGAGAGATTCTCGAGTTAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

Location/Qualifiers
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VATIKSVRFYTEKNGQLIYTPFTEDTPSVGQRLLNSVLNTLIMISVIVVMTIFLVVLY
KYRCYKFIHGWLIMSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLFLAVMNFGAVGMVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IHWKGPLVLQQAYLIVISALMALVFFKYLPPWSAWVIGAISVYDLVAVLCPKGPLRM
LVETAQERNEPIFPALIYSCEWSHASARHWGVSRWPFVEAWKWAVVLISDRLYILS"
486 c 598 g 479 t
                                                                                                     /organism="Mus musculus"
/mol type="mRNA"
strain="CS7BL/6J"
/db_xref="FANTOM_DB14833416A15"
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/db_xref="MO1:11909172"
/db_xref="MO1:11909172"
/tissue type="MO1:11909175"
/tissue type="Mo1:11909175"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="0 day neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MLAFMASDSEEEVCDERTSLMSAESPTSRSCQEGRPGPEGGEST/
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/note="unnamed protein product; presenilin 2
(MGD|MGI:109284, GB|NM_011183, evidence: BLASTN, 99%
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Matches:
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/protein_id="BAB29514.1"
/db_xref="GI:12852721"
/db_xref="MGI:109284"
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/lab_host="DH10B"
/clone_lib="NCI_CCAP_Pr28"
/note="Organ: prostate; Vector: pT773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and 8s
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Prepared by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1317 Std Brrox: 0.00
Beq primer: -40UP from Giber
High quality Sequence stop: 461.
High quality Sequence stop: 461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 bp mRNA linear EST 17-DEC-1999 wb97al2.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2313598 3' similar to SW:\(\overline{\text{PSN2}}\)\(\overline{\text{HUMAN}}\) P49810 PRESENILIN 2 ;, mRNA sequence. A1675803
                                                                                                                                                                                   202
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                                                                                                                              GACTATCCCACACTCTTCCTGGCTGTCTGGAACTTCGGGGCAGTGGCATGTGTGCATC 682
                                                                                                                                                                                                                                                           AlaLeuValPheileLysTyrLeuProGluTrpThrValTrpPheValLeuPheValIle 222
                                                                                                                                                                                                                                                                                                SerValTrpAspLeuValAlaValLeuThrProLysGlyProLeuArgTyrLeuValGlu 242
503 TACAAGTATCGATGCTACAAGTTCATCCATGGCTGGCTGATCATGTCCTCCCTGATGCTC 562
                                   LeuPheleuPheThrIleTyrValGlnGluValLeuLysSerPheAspValSerPro 162
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 661) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                   HisTrpLysGlyProLeuArgLeuGlnGlnPheTyrLeuIleThrMetSerAlaLeuMet
                                                                                                                                                                                                                                                                                                                                                                                                             243 ThrAlaGlnGluArgAsnGluProllePheProAlaLeulleTyrSer 258
                                                                                                                                                                                                                                                                                                                                                                                                                               863 ACTGCCCAGGAGAGAAATGAGCCCATATTTCCTGCCCTGATATACTCA 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'organism="Homo sapiens"
|mol_type="mRNA"
|db_xref="taxon:9606"
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BUG14355 697 bp mRNA linear EST 20-FEB-2003 UI-M-EVO-Cbf-1-22-0-UI.rl NIH BMAP_EVO Mus musculus cDNA clone UI-M-EVO-Cbf-1-22-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 GTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGAAGAATGGACAG---CTC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 LeuSerHisProPheValArgGluThrAspSerIleValGluLysGlyLeuMetSerLeu 102
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Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 697)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 LeuPheLeuPheThrThrIleTyrValGlnGluValLeuLysSerPheAspValSerPro 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 TACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCATGTCTTCATCATGATGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 CACTGGAAGGGCCCTCTGGTGCTGCAGGCCTACCTCATCATGATCAGTGCGCTCATG
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985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. " 190 c 166 g 171 t 2 others
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135
37
44
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Mismatches:
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Matches:
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222

202

423

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Email: Capbs-remail.nib.gy/
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bprp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 459.
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/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/loot="Togan: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand CDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Bco RI adaptors (Pharmacia), digested with Not I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1925372 TO SEP-1999 WHS3d06.xl NCI_CGAP_Lu19 Homo sapiens CDNA clone IMAGE:2449163 3' similar to SW:PSN2_HUMAN P49810 PRESENILIN 2 ;, mRNA sequence.
   163 SerAlaLeuLeuValLeuPheGlyLeuGlyAsnTyrGlyValLeuGlyMetMetCysIle 182
                                                                                                                                                                                                                                                                                                                                                                                                   484 GCCCTGGTATTTATCAAGTACCTCCCCGAATGGACCGCATGGCTCATCTTGGCTGTGATT 543
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                                                                                                                                                                                                                                                                              424 CACTGGAAAGGCCCCCTTCGACTGCAGCAGGCGTATCTCATTATGATCAGTGCCCTCATG 483
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="IMAGE="49163"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerValTrpAspLeuValAlaValLeuThrProLysGlyProLeuArgTyrLeuValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 ThrAlaGlnGluArgAsnGluProIlePheProAlaLeuIleTyrSerSerGlyValIle
                                                                                                                                  HisTrpLysGlyProLeuArgLeuGlnGlnPheTyrLeuIleThrMetSerAlaLeuMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 TyrProTyrValLeuValThrAlaValGlu 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        664 TGG-----TTGGTGAATATGGCTGAA 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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/tissue_type="wand-brain"
/dev stage="wand-brain"
/dev stage="wand-brain"
/dev stage="wand-brain"
/done lib="will BmAP Ev0"
/clone directionally into pix-Asc vector. The library tag sequence located between the Not I site and the polyA tail
/is GTGCTGGAA. This library was created for the
/wiversity of lows Mouse Brain Molecular Anatomy Project
/clone Discovery in the Developing Mouse Nervous
/clone lib="will BmAP"
/clone Discovery in the Developing Mouse Nervous
/clone will Chin, Ph.D., program coordinator."
/clone lib="will BmAP"
/clone lib="will BmAP"
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Contact: Robert Strausberg, Ph.D.
Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clohe Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                    This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 GTCGTCGTGGCCACCATCAAATCAGTTAGATTACCCGGAAGGACGGTCAG---CTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrLysTyrLysPheTyrLysLeulleHisGlyTrpLeulleValSerSerPheLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 LeuPheLeuPheThrThrIleTyrValGlnGluValLeuLysSerPheAspValSerPro 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 TTGAAATATGGAGCCAAGCATGTCATCATGTTTTTGTCCCCGTGACCCTCTGCATGGTC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
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   Institutes of Health, Mammalian Gene Collection (MGC)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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699.00
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29.39%
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Best Local Similari
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TITLE
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/tissue type="B CELLS (RAMOS CELL LINE)"
/cell line="RAMOS CELL LINE"
/cell line="RAMOS CELL LINE"
/colone lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Woetor: pcMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoxV sites of the pcMVSPORT 6 vector.
                                                                                                                               Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 105 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 595.f For
more information about this cluster, see
http://www.genoscope.com.fr/
cgi-bin/cluster.cgi?eq=CSOAGO04BH10NP1&cluster=595.f. Contact :
Feng Liang Enail : fliang@lifetech.com.URL :
Feng Liang Enail : fliang@lifetech.com.URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOAGO04BH10NP1.
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                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    963 AAGTICATCCATGGCTGGTTGATCATKICTTAACTGAGGCTGCTGTTCCTCTTCACCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 PheGlyLeuGlyAsnTyrGlyValLeuGlyMetMetCyBileHisTrpLysGlyProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 ArgieuGinGinPheTyrLeulleThrMetSerAlaLeuMetAlaLeuValPhelleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGCTGCAGGCCTACCTCATCATGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAG
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163
29
57
62
8
                                                                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
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Matches:
Conservative:
Mismatches:
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DG004Y020"
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688.50
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Best Local Similarity:
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SOURCE
ORGANISM
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                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaLeuValPheIleLysTyrLeuProGluTrpThrValTrpPheValLeuPheValIle 222
                                                                                                                                                                                                                                                                                                                                                                                                                                        185 CTGAACACCCTCATCATGATCAGGGTCATGGTGGTTATGACCATCTTTGGTGGTGCTC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyriysTyriysPheTyriysLeuileHisGlyTrpLeuileValSerSerPheLeuLeu 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCATGTCTTCACTGATGCTG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuSerHisProPheValArgGluThrAspSerIleValGluLysGlyLeuMetSerLeu 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 GlyAsnAlaLeuValMetLeuCysValValValLeuMetThrValLeuLeulleValPhe 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HisTrpLysGlyProLeuArgLeuGlnGlnPheTyrLeuIleThrMetSerAlaLeuMet 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThralaGinGluArgAsnGluProllePheProAlaLeulleTyrSerSerGlyValile 262
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                                                                                                                                                                                                                                                                                                       CTCAAATACTTAGCGAAGCACGTGATCATGCTGTTTGTGCCTGTCACTGTGCATGATC 67
                                                                                                                                                                                                                                                                                                                                                    LeuValValPheThrMetAsnThrIleThrPheTyrSerGlnAsnGlyArgHisLeu 82
                                                                                                                                                                                                                                                                                    LeulysTyrGlyAlaSerHisVallleHisLeuPheValProValSerLeuCysMetAla 62
modified
cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went througb one round of normalization. Library constructed by Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerValTrpAspLeuValAlaValLeuThrProLysGlyProLeuArgTyrLeuValGlu
                                                                1 others
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134
40
1
                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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                                                                184
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                                               Fatima Bonaldo. '
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                                                                                                                             2.6e-59
698.50
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                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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TGG 667
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Pred. No.:
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

Emmert-Buck, M.D., Ph.D.

Emmert-Buck, M.D., Ph.D.

EDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llni.gov/bbrp/fmage/fmage.html

Insert Length: 1711 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 456.
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1 (bases 1 to 680)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished
                                                                                             503 GAGCCCATATTCCCTGCCCTGATATACTCATCTGCCATGGTGTGGACGGTTGGCATGGCG
                                                                --- AlaValGluAsnThrThrAspProArg---GluPro
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/dev stage="adult"
/lab_host="bH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
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/done_lib="WICGAP_LN19"
/note="Organ: lung; Vector: pT713D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I -oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.

Fatima Bonaldo. In 178 the strand of the strand Promobile Processing Processing Normalization and M. In the strand Processing Normalization and M. In the strand Processing Normalization and M. In the strand Processing Normalization and M. In the strand Processing Normalization and M. In the strand Processing Normalization and M. In the strand Processing Normalization and M. In the strand Processing Normalization and M. In the strand Processing Normalization and M. In the strand Processing Normalization and M. In the strand Processing Normalization and M. In the strand Processing Normalization and M. In the strand Processing Normalization and M. In the strand Processing Normalization and M. In the strand M. In
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                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 881)

NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                    Uppublished
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llhl.gov
Plate: NDAM462 row: m column: 02
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/clone="IMAGE:30389377"
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Tumour suppressor
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Full AD4/AD3LP seq
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C elegans sel-12 g
Human S182 gene, P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 ATGCCTTCCACAAGGAGACAACAGGAGGCGGAGGTGCAGATGCGGAAACACATACCGTT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 TyrGlyThrAsnLeuIleThrAsnArgAsnSerGlnGluAspGluAsnValValGluGlu 40
                                                                                                                                                                                                                                                                                                                                                                          The sel-12 gene (AAT60106) of Caenorhabditis elegans (CE) encodes a polypeptide (AAM14006) that displays about 50% amino acid sequence defentity to human presentiin PS1 and PS2 proteins associated with Alzheimer's disease (AD). Like presentiins, sel-12 is widely expressed in neural and non-neural cells. The gene was identified by Streening for suppressors of the 'Multivulva' phenotype of CE caused by an allele of lin-12 that causes constitutive LiN-12 cativation. 2 Recessive suppressors, ar131 and ar133, proved to be alleles of the new gene (sel means suppressor and/or enhancer of lin-12). The gene can be used to produce wild-type or mutated (see lin-12). The gene can be used to produce wild-type or mutated (see also AMM14007) SEL-12 in host cells, in methods for screening for extragenic suppressors or enhancers of a SEL-12 allele, and in the development of transgenic annimals, esp. transgenic CE, useful in
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                                                                                                                                                                                                                                                                    the diagnosis and prophylactic or therapeutic treatment of disorders such as Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to DNA molecules comprising the promoter of the sel-12 gene from Caenorhabditis elegans operably linked to a heterologous DNA sequence encoding a protein of interest. The sequence can be used to develop drugs for the treatment, prevention or delay of a neuronal disorder. In particular, the neuronal disorder may be familial Alzheimer's disease. The present sequence is the C. elegans sel-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ThrValTyrGlyThrAsnLeuIleThrAsnArgAsnSerGlnGluAspGluAsnVa
                                                                                                                                                                                                                                                                                                                                   Isolated DNA molecule comprising promoter of the sel-12 gene from Caenorhabditis elegans operably linked to heterologous gene, directs expression in neural cells and is useful to develop drugs to treat
                                                                                                            Sel-12, presenilin, neuronal disorder, familial Alzheimer's disease, amyloid precursor protein, APP, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4137 BP; 1252 A; 770 C; 703 G; 1412 T; 0 other;
                                                                                        C elegans sel-12 gene promoter and regulatory regions.
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3238
                                                                           2340 AATTTCAGCTTCTACAGCTTTTCCTGGAGAGGCGAGTTGTTCATCTGAAAAGCGCAAAAGG 2399
                                                                                                                                        2400 GCCAAAAGTGAAACGAATTCCTCAAAAAGTGCAAATCGAATCGAATACTACAGCTTCAAC 2459
                                                                                                                                                                                                                                     25.0 AGACGCCAATTTTCACAGGCACGAAGAGGAAGAGAG-TGAGTGAAAAAACGTGCTGAAAAA 2578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   423 hrPheValProAlaGlySerSerProHisLeuLeuHisLysSerLeuLysSerValTyrT 443
                                     287 -----Thr-SerThrAlaPheProGlyGluAlaSerCysSerSerGluThrProLysAr 304
                                                                                                                 304 gProLysValLysArglleProGlnLysValGln1leGluSerAsnThrThrAlaSerTh 324
                                                                                                                                                                                               324 rThrGlnAsnSerGlyValArgValGluArgGluLeuAlaAlaGluArgProThrValGl 344
                                                                                                                                                                                                                                                                            nAspAlaAsnPheHisArgHisGluGluGluGluArg-------356
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The present sequence represents the human S182 gene, FS1 locus. Mutant PS1 produces a gene product that increases the probability of Alzahamer's disease. Possible mutations of the PS1 locus are shown in the features table. A nucleic acid sequence able to hybridise to sequences coding for a mutant PS1 polypeptide can be used as probes for diagnosing an increased likelihood of contracting Alzhahamer's disease. Alzhodimer sequences containing or expressing a nucleic acid molecule, protein or antibody specific for mutant PS1 can be administered to a protein to rantbody specific for mutant PS1 can be administered to a prient to reduce the likelihood, or delay the onset, of Alzheimer's disease, e.g. anti-sense RNA expression can be used to decrease alzheimer's disease protein can be used to decrease chrements disease protein can be used to test candidate therapeutics and to investigate the normal role of PS1. The PS1 peptide may also be included in pharmaceutical compositions (vaccines) for Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chromosome 14 early-onset familial Alzheimer's disease gene PS1 mutants - useful for diagnosing likelihood of developing Alzheimer's disease, also anti-sense sequences, antibodies and vaccines to delay
                                                                                                                                                                                                                                               c
"A mutated form of PS1 has t replacing the
wild-type c at this position"
                                                                                                                                                                                                                                                                                                       d
"A mutated form of PS1 has a replacing the
wild-type g at this position"
                                                                                                                                                                                                 "A mutated form of PS1 has c replacing the wild-type t at this position"
                                         Mutant; antiBense; antibody; vaccine; Alzheimer's diBease; ds
      Human S182 gene, PS1 locus, related to Alzheimer's disease
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                                                                                                    Location/Qualifiers
                                                                                                                                                    product= PS1
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                                                                          Homo Bapiens,
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                                                                                                                                                                                                                                                                                             mutation
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                                                                                                                                                                                                                                mutation
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Seguence 2765 BP; 715 A; 625 C; 652 G; 772 T; 1 other;

disease therapy

2765 215 75 107 48

Conservative: Mismatches: Indels:

6.16e-90 994.50 65.17% 48.31% 41.82%

Best Local Similarity: Query Match: DB:

Percent Similarity:

Alignment Scores:

Length: Matches:

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95US-0002448.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTCCAGCTCTCATTTACTCCTCAACAATGGTGTGG------TTGGTGAATATGGCA 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 GlyValLySLeuGlyLeuGlyAspPhellePheTyrSerValLeuLeuGlyLysAlaSer 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 ProGlyGluAlaSerCysSerSerGluThrProLysArgProLysValLysArgllePro 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 ArgProThrValGlnAspAlaAsn-----PheHisArgHisGluGluGluGluArg 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluTrpThrValTrpPheValLeuPheValIleSerValTrpAspLeuValAlaValLeu 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 PheProAlaLeuileTyrSerSerGlyValIleTyrProTyrValLeuValThrAlaVal 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 GlnLysValGln11eGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg 331
                                                                                                                                                                                                                                                                                                                                                     192 GlnPheTyrLeuIleThrMetSerAlaLeuMetAlaLeuValPheIleLysTyrLeuPro 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluAsnThrThrAspProArgGluProThrSerSerAspSerAsnThrSerThrAlaPhe 291
                                              138 GAGCAAGATGAGGAAGAAGAAGATGAGGCTGACATTGAAATATGGGGGCCAAGCATGTGATC 497
                                                                                       558 AGCTITITATACCCGGAAGGATGGGCAG---CTAATCTATACCCCATTCACAGAAGATACC 614
                                                                                                                                                                              92 AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal 111
                                                                                                                                                                                             615 GAGACTGTGGGCCAGAGACCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTC 674
                                                                                                                                                                                                                                   112 ValValLeuMetThrValLeuLeulleValPheTyrLysTyrLysPheTyrLysLeulle 131
                                                                                                                                                                                                                                               132 HisGlyTrpLeuIleValSerSerPheLeuLeuLeuPheLeuPheLThrIleTyrVal 151
                                                                                                                                                                                                                                                                                                152 GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171
                                                                                                                                                                                                                                                                                                                                                                                           172 GlyasnTyrGlyvalLeuGlyMetMetCysIleHisTrpLysGlyProLeuArgLeuGln 191
                                                                                                                          72 ThrphelyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr 91
                       32 GlnGluAspCluAsnValValGluGluAlaGluLeuLysTyxGlyAlaSerHisValIle 51
                                                                         52 HisLeuPheValProValSerLeuCysMetAlaLeuValValPheThrMetAsnThrIle 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AD3; AD4/AD3LP; Alzheimer's disease; chromosome; missegregation; presenilin; inhibitor; AD; trisomy 21; ss.
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                                                                                                                                                               ValvalLeuMetThrValLeuLeulleValPheTyrLysTyrLysPheTyrLysLeulle 131
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                                                                                                                                                                                                                                                  AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal 111
                                                                                                                   11 GAGCAAGATGAGGAAGAAGAAGAAGAGCTGACATTGAAATATGGCGCCAAGCATGTGGATC 70
                                                                                                                                                  HisLeupheValProValSerLeuCysMetAlaLeuValValPheThrMetAsnThrIle 71
                                                                                                                                                                                                 ThrpheTyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr 91
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              Conservative:
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                                                                                                                                                                                                                                                                                                        395 LeuCysPheThrLeuValLeuLeuAlaValPheLysArgAlaLeuProAlaLeu-GlnPh 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 uHisLysSerLeuLysSerValTyrTyrIleAsnSerLeuPhe------LeuProPh 451
357 GlyvalLysLeuGlyLeuGlyAspPheIlePheTyrSerValLeuLeuGlyLysAlaSer
                                                                                                                                                                                                    377 SerTyrPhe----AspTrpAsnThrIleAlaCysTyrValAlaIleLeuIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 eProPheSerProAspSerPhePheThrPheValProAlaGlySerSerProHisLeuLe
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Alzheimer's disease; mitochondrial pathology; neurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding presenilin peptide PS1/429 and its analogues - useful diagnosis and treatment of Alzheimer's disease
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generally useful as probes for detection and quantification of PS1/429, particularly for diagnosis of AD, especially the target sequences that hybridise with probes are isolated for sequencing. Antibodies (Ab) can also be diagnosed at the protein level using Ab as immunoassay reagents. Ab can also be used to identify epitopes and for affinity purification of peptides. Antisense nucleic acid may also be used to regulate expression of the PS1/429 gene, and both nucleic acids and peptides are useful as size markers in electrophoresis, chromatography etc. The transgenic animals are used as models for AD, e.g. for testing druges. Regulators of the PS1/429 gene or polypeptide can be used to treat e.g. AD or diseases involving mitochondrial pathology, apoptosis and neurodegeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 ThrProLysGlyProLeuArgTyrLeuValGluThrAlaGlnGluArgAsnGluProlle 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGACTGTGGGCCAGAGAGCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTC 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             644 TGGAATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAG 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 AGCTTTTATACCCGGAAGGATGGGCAG---CTAATCTATACCCCATTCACAGAAGATACC 403
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                                                                                                                                                                                                                          Typical regulators are antisense sequences, ribozymes, aptamers, synthetic or natural compounds. (II) may also be used to target other
                                                                                                                                                                                                                                                                                                         Sequence 1703 BP; 434 A; 372 C; 418 G; 479 T; 0 other;
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1004 -------GAGTCACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAGT 1048
                                                                                                                                                                                                                                      1049 GAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTCA 1108
                                                                                                                                                                                                                                                                                     1229 GCAACAGCCAGTGGAGTGGAACACAACATAGCCTGGTTTCGTAGCCATATTAATTGGT 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1349 TCCA---TCACCTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTACAGCCTTTT 1405
                                                                                                                                                                                                         ------ArgGluLeuAlaAlaGlu 339
                                                                                                                                                                                                                                                                     340 ArgProThrValGlnAspAlaAsn-----PheHisArgHisGluGluGluGluArg 356
                                                                                                                                                                                                                                                                                                                            357 GlyValLysLeuGlyLeuGlyAspPheIlePheTyrSerValLeuLeuGlyLysAlaSer 376
                                                                                                                                                                                                                                                                                                                                                                                        377 SerfyrPhe-----AspTrpAsnThrThrIleAlaCysTyrValAlaileLeulleGly 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuCysPheThrLeuValLeuLeuAlaValPheLysArgAlaLeuProAlaLeu-GlnPh 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 eproPheSerProAspSerPhePheThrPheValProAlaGlySerSerProHisLeuLe 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 uHisLysSerLeuLysSerValTyrTyrIleAsnSerLeuPhe------LeuProPh 451
                                                                                      292 ProGlyGluAlaSerCysSerSerGluThrProLysArgProLysValLysArgIlePro 311
                                                                                                                                                312 GlnLysValGlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg 331
884 TITICCAGCICTCATITACTCCTCAACAATGGTGTGG------TTGGTGATATGGCA 934
                            272 GluasnThrThrAspProArgGluProThrSerSerAspSerAsnThrSerThrAlaPhe 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Presenilin peptide; PS1/429; immunogen; immune response; PS1 gene;
Alzheimer's disease; mitochondrial pathology; neurodegeneration;
                                                                                                         935 GAAGGAGCCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
249..1652
                                                                                                                                                                                                           332 ValGlu-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS1/467 protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV17358 standard; DNA; 2764 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US09272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0683315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis; PS1/467; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ното варіепв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-1997;
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us-09-043-944-1.rng

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This sequence encodes the PS1/467 presentlin peptide. This sequence is specifically stated as not being in the nucleic acid of the invention, which encodes the PS1/429 presentlin peptide PS1/429 (II). Cells transformed with the DNA are used to produce recombinant (II) and analogues, useful e.g. as immunogens for generating an immune response against PS1/429. (II) is a mew product of the PS1 gene, mutations in which cause Alzheimer's disease (AD). The nucleic acids are generally useful as probes for detection and quantification of PS1/429, and probes are isolated for sequencing. Antibodies (Ab) can by bridise with probes are isolated for sequencing. Antibodies (Ab) can also be used to identify epitopes and for affinity purification of peptides. Antisense nucleic acid may also be used to regulate expression of the PS1/429 gene, and both nucleic acids and peptides are useful as size markers in electrophoresis, chromatography etc. The transgenic chimals are used as models for AD, e.g. for testing drugs. Regulators of the PS1/429 gene or polypeptide can be used to treat e.g. AD or diseases involving mitochondrial pathology, apoptosis and neurodegeneration.

Typical regulators are antisense sequences, ribozymes, aptemers, syntheric or natural compounds. (II) may also be used to target other coding sequences to particular cellular locations.
                                                                                                                                                                                                                   DNA encoding presenilin peptide PS1/429 and its analogues - useful for diagnosis and treatment of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2764 BP; 715 A; 624 C; 653 G; 772 T; 0 other;
                                                                                                                                                                                                                                                                                        Disclosure, Fig 2; 77pp; English.
                                                                                                   Drache
    96US-0659296
                                                                                                Davis JN,
                                                                                                                                             WPI; 1998-042186/04.
                                               (FARB ) BAYER CORP.
  06-JUN-1996;
                                                                                            Chisholm JC,
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2764 216 77 104 48 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 7.78e-90 993.50 65.84% 48.54% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

438 GAGCAAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATC 497 AGCTITTATACCGGAAGGAIGGGCAG---CTAAICTAIACCCCAITCACAGAAGAIACC 614 GAGACTGTGGGCCAGAGAGCCCTGCACTCTGAATGCTGCATGCTGCAGTGTC 674 HisGlyTrpLeuileValSerSerPheLeuLeuLeuPheLeuPheThrThrileTyrVal 151 GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171 32 GlnGluAspGluAsnValValGluAlaGluAlaGluLeuLySTyrGlyAlaSerHisVallle 51 52 HisLeuPheValProValSerLeuCysMetAlaLeuValValPheThrMetAsnThrIle 71 Thr Phe Tyr Ser Gln Asn Asn Gly Arg His Leu Leu Ser His ProPhe Val Arg Glu Thr 91 AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal ValValLeuMetThrValLeuLeulleValPheTyrLysTyrLysPheTyrLysLeulle US-09-043-944-1 (1-461) x AAV17358 (1-2764) 498 72 558 85 615 112 675 735 132 152 à g ò q ò g à qq à d g à

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131

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qq	795	:::::::: ::: GGGBABGTGTTTAAAACCTATACGTGCGACTACATTACTGTTGCACTCCTGATC 854
ò	172	GlyAsnTyrGlyValLeuGlyMetMetCysIleHisTrpLysGlyProLeuArgLeuGln 191
g	855	TGGAATTTTGGTGTGGGAATGATTTCCATTCACTGGAAAGGICCACTTCGACTCCAG 914
S A	192	GInPheTyrLeuIleThrMetSerAlaLeuWetAlaLeuValPheIleLysTyrLeuPro 211
ò	212	eu 23
q	975	- C
à	232	ThrProLysGlyProLeuArgTyrLeuValGluThrAlaGlnGluArgAsnGluProlle 251
g	1035	TGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTT 1094
à	252	PhebroAlaLeulleTyrSerGlyVallleTyrProTyrValLeuValThrAlaVal 271
Q	1095	tcatttactcctcacaarggrgrgg
ò	72	묜
g	1146	GAAGGAGACCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCC 1187
ò	292	roGlyGluAlaSerCysSerSerGluThrProLysArgF
g	1188	
ò	312	nLysValGlnIl
g	1215	1
à	332	ValGluArgGluLeuAlaAlaGlu 339
요	1260	GAGGAAIGGGAAGCCCAGAGGGACAGTCAICIAGGGCCTCATCGCTCTACACCTGAGTCA 1319
ð	340	ArgProThrValGlnAspAlaAsnPheHisArgHisGluGluGluGluArg 356
g	1320	AGACCCAGAGGAAAGG
ŏ	357	GlyValLysLeuGlyLeuGlyAspPheIlePheTyrSerValLeuLeuGlyLysAlaSer 376
g	1380	GGRGTAAAACTIGGATIGGGAGATITCATITICIACGGTICTGGTIGGTAAAGCCTCA 1439
ò	377	SerTyrPheAspTrpAsnThrThrIlealaCysTyrValalaIleLeuIleGly 394 :::
q	1440	
5 5	395	14
ò	14	CCAGCICITCCARIC 15
q	09	AGCCTTT
δλ	434	ValTyrTyr11eAsnSerLeuPheLeuProPh 451
g	1617	::: :: CGGTTAGAATCCCATG 16
ò	451	eLeuCysilelle 455
g		GAIGTTTCTTCTT 1689
RESULTANTO	r 7 323 AAL47323	standard; DNA; 2764 BP.
\$ \$ \$	AAL47323;	

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Isolated DNA molecule comprising promoter of the sel-12 gene from Caenorhabditis elegans operably linked to heterologous gene, directs expression in neural cells and is useful to develop drugs to treat
                                  Sel-12; presenilin; neuronal disorder; familial Alzheimer's disease; amyloid precursor protein; APP; ds.
                                                                                                      /product= "presenilin"
                                                                              Location/Qualifiers
249..1652
                                                                                                                                                             97US-0832867
                                                                                                                                                                              97US-0832867
                 Presenilin coding sequence
(first entry)
                                                                                               /*tag= a
                                                                                                                                                                                               (ELEG-) ELEGENE GMBH
                                                                                                                                                                                                                                 WPI; 2002-478281/51.
                                                                                                                                                                                                                                                                                      neuronal disorders
                                                                                                                                                                                                                                          P-PSDB; AA018049.
                                                                                                                                                                                                                 Baumeister R:
                                                                                                                                                             04-APR-1997;
                                                                                                                                                                              04-APR-1997;
                                                            Unidentified
                                                                                                                        JS6376239-B1
02-SEP-2002
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The present invention relates to DNA molecules comprising the promoter of the sel-12 gene from Caenorhabditis elegans operably linked to a heterologous DNA sequence encoding a protein of interest. The sequence and be used to develop drugs for the treatment, prevention or delay of a neuronal disorder. In particular, the neuronal disorder may be familial Alzheimer's disease. The present sequence is a presentin coding sequence described in the exemplification of the invention. Claim 2; Fig 4; 78pp; English.

Sequence 2764 BP; 715 A; 624 C; 652 G; 773 T; 0 other;

614 138 GAGCAAGATGAGGAAGATGAGGAGCTGACATTGAAATATGGGGCCAAGCATGTGATC 497 92 AspSerIleValGluLySGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCySVal 111 112 ValValLeuMetThrValLeuLeuIleValPheTyrLysTyrLysPheTyrLysLeuIle 131 71 91 S58 AGCTTTTATACCCGGAAGGATGGGCAG---CTAATCTATACCCCATTCACAGAAGATACC 32 GlnGluAspGluAsnValValGluGluAlaGluLeuLysTyrGlyAlaSerHisValIle HisLeuPheValProValSerLeuCysMetAlaLeuValValPheThrMetAsnThrIle ThrPheTyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr 2764 216 77 104 48 Conservative: Mismatches: Indels: Length: Matches: Gaps: US-09-043-944-1 (1-461) x AAL47323 (1-2764) 7.78e-90 993.50 65.84% 48.54% 41.78% Percent Similarity: Best Local Similarity: Alignment Scores: 72 Query Match: DB: 셤 8 a 8 g ò ò

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975 daarddachdcdredrentringcrentariricagrarardarrhadredechdrifig 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                           1035 TGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGGCTCAGGAGAAATGAAACGCTT 1094
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                                                                        GluTrpThrValTrpPheValLeuPheValIleSerValTrpAspLeuValAlaValLeu 231
                                                                                                                                                                                                                                                                                                                                                                                                        PheProAlaLeuIleTyrSerSerGlyValIleTyrProTyrValLeuValThrAlaVal 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 GluAsnThrThrAspProArgGluProThrSerSerAspSerAsnThrSerThrAlaPhe 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 GlnLysValGlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg 331
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HisGlyTrpLeuIleValSerSerPheLeuLeuLeuPheLeuPheThrThrIleTyrVal 151
                                                                                                                        GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171
                                                                                                                                               795 GGGGAAGTGTTTAAAAACCTATAAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATC 854
                                                                                                                                                                                                                                                                GlnPheTyrLeulleThrMetSerAlaLeuMetAlaLeuValPheIleLysTyrLeuPro 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 eProPheSerProAspSerPhePheThrPheValProAlaGlySerSerProHisLeuLe 434
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                                                                                                                                                                                                              GlyAsnTyrGlyValLeuGlyMetMetCysIleHisTrpLysGlyProLeuArgLeuGln
                                                                                                                                                                                                                                                                                    915 CAGGCATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT40028 and AAT40029 represent the coding sequences for the two different forms of wild type human presentlin-1 [PS-1]. The form represented by AAT40029 results from alternate splicing of the genomic DNA sequence. AAT40031 represents the coding sequence for wild type human PS-2. The presentlins are a family of highly conserved integral membrane proteins with a common structural motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in these sequences can be used for diagnosis of these diseases. The encoded proteins, or vectors that express them or containing antisense sequences, antibodies selective for mutant forms of
                                                                                                                                                                                                                                                                                              Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the encoded proteins (such as AAN05736) and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for durg screening. The antibodies can also be used e.g. for affinity purification and in immunoassays. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New presention genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2765 BP; 715 A; 624 C; 652 G; 773 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rommers JM;
                                                                                                                                                                                                                                                          Presenilin-1-1 wild type coding sequence.
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/product= presenilin-1-1
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249..1652
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1677 GATGTTTCTTCTT 1689
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P-PSDB; AAW05733.
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22-JUL-1997
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                                                                                                                                           AAT40028;
                                           RESULT 8
                                                                      AAT4002
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2765 216 77 104 48

Matches: Conservative: Mismatches:

Indels:

Length:

7.78e-90

Alignment Scores:

993.50 65.84% 48.54% 41.78%

Percent Similarity: Best Local Similarity: Query Match:

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1260 GAGGAÁTGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTCA 1319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 GlyasnTyrGlyValLeuGlyMetMetCysIleHisTrpLysGlyProLeuArgLeuGln 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 GluTrpThrValTrpPheValLeuPheValIleSerValTrpAspLeuValAlaValLeu 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 GlnLysValGInIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg 331
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                                                                                                                                                                                                                                                      91
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                                                                                                                                                                                                                                                                                         152 GlnGluValLeuLysSerPheAspValSerProSerAlaLeuValLeuPheGlyLeu
                                                32 GlnGluAspGluAsnValValGluGluAlaGluLeuLysTyrGlyAlaSerHisValIle
                                                                                                                                                                                                                                                      72 ThrPheTyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr
                                                                                                                                                                                                                                                                                                                                                          92 AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 ArgProThrValGlnAspAlaAsn-----PheHisArgHisGluGluGluGluArg
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US-09-043-944-1 (1-461) x AAT40028 (1-2765)
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/note= "absence of exon 9 through splicing variation, results in Asp.257 changing to Ala and fusion of Ala-257 to Thr-291"
                                                        /note= "deletion of 12 nucleotides from 3' end o
exon 4 by alternative splicing, deletes
Val26-Gln-29 (not critical to PSI
                                                                                                                                                                   '*tag= q
'note= "T to C FAD mutation site (Tyrll5His)"
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"T to C FAD mutation site (Ile143Thr)"
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note= "A to C FAD mutation site (Met146Leu)"
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note= "C to T FAD mutation site (Ala260Val)"
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note= "C to T FAD mutation site (Ala285Val)"
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'note= "G to C FAD mutation site (Gly384Ala)"
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/note= "A to G FAD mutation site (lle439Val)"
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note= "G to A FAD mutation site (Cys410Tyr)"
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                                                                                                   377 SerTyrPhe-----AspTrpAsnThrThrIleAlaCysTyrValAlaIleLeuIleGly 394
                                                          LeuCysPheThrLeuValLeuLeuAlaValPheLysArgAlaLeuProAlaLeu-GlnPh 414
                                                                                         414 eProPheSerProAspSerPhePheThrPheValProAlaGlySerSerProHisLeule 434
                                                                                                                          434 uHisLysSerLeuLysSerValTyrTyrIleAsnSerLeuPhe-----LeuProPh 451
                                                                                                                                                                                                                                                                         Presenilin-1; PSI gene; human; familial Alzheimer's disease; FAD; cerebral haemorrhage; schizophrenia; depression; epilepsy; mental retardation; diagnosis; therapy; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
249..1652
                                                                                                                                                                                                                                                         Human presenilin-1 cDNA (hPS1-1).
                                                                                                                                                                                                          AAV04666 standard; cDNA; 2765 BP
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/number= 9
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/*tag= j
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                                                                                                                                                                                                                                                                                                                                                              This cDNA clone, deposited as ATCC 97124, codes for human

presentin-1 (hPS1, see AAW23964). Mutations in the presentin genes

Alzheimer's disease (FAD) and may be causative of corns of familial

Alzheimer's disease (FAD) and may be causative of cher disorders,

c.g. cognitive, intellectual, neurological or physiological

disorders such as cerebral haemorrhage, schizophrenia, depression,

mental retardation and epilepsy. Isolation of the hPSI cDNA

mental retardation and epilepsy. Isolation of the hPSI construction

c.g. cognitive mapping of the AD3 region, transcription mapping

and analysis of candidate genes, and recovery of candidate genes by

CC a physical contig spanning the AD3 region, transcription mapping

and analysis of candidate genes, and recovery of candidate genes by

CC a physical contig spanning the AD3 region, transcription mapping

and analysis of candidate genes, and recovery of candidate genes by

CC are AAV04668) and a human presentin-2 sequence (see AAV04669) are

also provided, as well as genomic sequences for hPSI (see

AAT99661-71). Use of the mucleic acids and proteins comprising or

c derived from the presentlins is made in screening and diagnosing

CC FAD, identifying and developing therapeutics for treatment of FAD,

and in producing cell lines and transgenic animals useful as models

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                                                                                                                                                                                                                                           New isolated mutant presention-1 genes - useful for developing products for use in detection, diagnosis and therapy of Alzheimer's disease and for drug screening
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                Disclosure; Page 178-180; 238pp; English.
                                                                HSC RES & DEV LP.
UNIV TORONTO GOVERNING COUNCIL.
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  96US-0021700
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Percent Similarity:
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12-JUL-1996;
08-NOV-1996;
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395 LeuCysPheThrLeuValLeuLeuAlaValPheLysArgAlaLeuProAlaLeu-GlnPh 414
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                                     GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 GAGCAAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCCAAGCATGTGATC 497
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                                                                                     Human; catenin p120; presenilin-1; PS-1; neuroprotective; gene therapy; neurodegenerative disease; Alzheimer's disease; nootropic; prophylaxis; neuronal disorder; cognitive disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                             modulating presentlin-catenin p120 interaction and thus for treating cognitive disorder e.g., Alzheimer's disease comprises enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying presentlin or catenin p120 activity modulator useful for
                                                                                                                                                                                                           /product= "Human presenilin-1 protein"
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                                                                 Human presentlin-1 (PS-1) protein DNA
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                                                                                                                                                                  cocation/Qualifiers
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Best Local Similarity:
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-440 GCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCATATTAATTGGT
72 ThrPheTyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr
                                                                      558 AGCTITITATACCCGGAAGGATGGGCAG---CTAATCTATACCCCATTCACAGAAGATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 GlnPheTyrLeuIleThrMetSerAlaLeuMetAlaLeuValPheIleLysTyrLeuPro
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1260 GAGGAÁTGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATÓGCTCTACACCTGAGTCA 1319
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                                                                                                                                                                                              GlnGluAspGluAsnValValGluGluAlaGluLeuLysTyrGlyAlaSerHisValIle
                                                                                                                 GAGCAAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATC
                                                                                                                                                                   HisLeuPheValProValSerLeuCysMetAlaLeuValValPheThrMetAsnThrIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes human presentlin 1. KIAA0253 binds to presentlin. The specification describes a method of identifying a modulator of presentlin function or KIAA0253 function. The method comprises determining presentlin activity or KIAA0253 activity in the presence and absence of a test compound, where presentlin activity is determined by its ability to bind to KIAA0253. A modulator of presentlin or KIAA0253 polypeptide is useful in the manufacture of a medicament for the treatment or prophylaxis of Alzheimer's disease. The KIAA0253 polymucleotide and KIAA0253 polypeptide are useful in the treatment, prophylaxis or diagnosis of Alzheimer's disease.
                                    eProPheSerProAspSerPhePheThrPheValProAlaGlySerSerProHisLeuLe
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P-PSDB; AAG63936.
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Best Local Similarity:
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                                    SerTyrPhe-----AspTrpAsnThrThrIleAlaCysTyrValAlaIleLeuIleGly 394
                                                                                 LeuCysPheThrLeuValLeuLeuAlaValPheLysArgAlaLeuProAlaLeu-GlnPh 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A full-length cDNA (AATS9536) of the early onset Alzheimer's disease (BOAD) splice variant gene sequence codes for a 463-amino acid polygeptide (AAM1839). Another full-length cDNA (AATS9535) of the EOAD gene codes for a 467-amino acid polypeptide (AAM1840). The 2 sequences can be used to generate primers and probes for the diagnosis of predisposition to Alzheimer's disease, esp. EOAD.
                                                                                                                                                                                                                                                                                                                                                                          Human early onset Alzheimer's disease (EOAD) splice variant gene.
                                                                                                                                                                                                                                                                                                                                                                                                 Early onset Alzheimer's disease; EOAD; neurodegenerative disease;
diagnosis; gene therapy; antisense; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Early onset Alzheimer's disease gene - useful for diagnosing
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They can also be used for prodn. of EOAD polypeptides in transformed host cells, and antisense sequences can be used for the treatment of EOAD.
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                                       A full-length cDNA (AAT59535) of the early onset Alzheimer's disease (BOAD) gene sequence codes for a 467-amino acid polypeptide (AAW11839). Another full-length cDNA (AAT59516) of an BOAD splice variant gene codes for a 463-amino acid polypeptide (AAW11840). The 2 sequences can be used to generate primers and probes for the diagnosis of predisposition to Alzheimer's disease, esp. BOAD. They can also be used for prodn. of BOAD polypeptides in transformed host cells, and antisense sequences can be used for the treatment of BOAD.
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osis; gene therapy; antisense; ds.
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1365 GCAACAGCCAGTGGAACTGGAACACAAACCATAGCCTGTTTTGTAGCCATATTAATTGGT 1424
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                                                                                                                               -------GAGTCACAGACACTGTTGCAGAGAATGATGATGGTGGGGGTTCAGT 1184
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                                                                                                                                                                                                                                                                                                    GlyValLysLeuGlyLeuGlyAspPheIlePheTyrSerValLeuLeuGlyLysAlaSer 376
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1071 GAAGGAGACCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCC----
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The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA dity analysis as given in the specification, and comparing the expression level in an unactivated the expression level in an unactivated comparing the expression level in an unactivated (GCA). Also included are modulating (M2) GA by contexting GCA with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject; exposure of a subject to a pathogen or sterile inflammatory disease using the cubject to a pathogen or sterile inflammatory disease, by detecting the cubject to a pathogen or sterile inflammatory disease, by detecting the cubject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene (8) from GS, where complete the expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene (8) from GS in the tissue. M1 is useful for detecting a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatory distress syndrom; unjury, ARDS, adult respiratory distress syndrom; or inflammatory bowel disease, crohic disease, ulcerative colitis, periodottal disease, also bacterial infection, viral infection, and M5 is
Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                        Claim 1; SEQ ID No 483; 114pp; English.
                                                                                                   drug toxicity
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Sequence 3056 BP; 762 A; 688 C; 740 G; 866 T; 0 other;

3056	216	16	105	48	0
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2.29e-89	989.50	65.62%	48.54%	41.61%	24
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US-09-043-944-1 (1-461) x ABK83912 (1-3056)

	32	32 GlnGluAspGluAsnValValGluGluAlaGluLeuLysTyrGlyAlaSerHisValIle 51
	731	::::: 731 GAGCAAGATGAGGAAGAAGATGAGAGCTGACATTGAAATATGGCGCCAAGCATGTGATC 790
	52	52 HisLeuPheValProValSerLeuCysMetAlaLeuValValPheThrMetAsnThrIle 71
•	791	AIGCICTITIGICCCTGIGACTCTCTGCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG
	72	72 ThrPheTyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr 91
	851	
	92	92 AspSerIleValGluLysGlyLeuMetSerLeuGlyAspAlaLeuValMetLeuCysVal 111
•	806	GAGACTGTGGGCCCAGAGAGCCCTGCATTCTGAATGCTGCCATCATGATCAGTGTC 967
	112	112 ValValfeuMetThrValLeuLeuIeValPheTyrLysTyrLysPheTyrLysLeuIle 131

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1088 GGGGAAGTGTTAAAACCTATAACGTTGCTGGACTACATTACTGTTGCACTCCTGATC 1147
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                                                                                                                                                                                 GlnPheTyrLeuIleThrMetSerAlaLeuMetAlaLeuValPheIleLysTyrLeuPro 211
                                                                                                                                                                                                                                  GluTrpThrValTrpPheValLeuPheValIleSerValTrpAspLeuValAlaValLeu 231
                                     HisGlyTrpLeuIleValSerSerPheLeuLeuPheLeuPheThrThrIleTyrVal 151
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                                                                                                                                   172 GlyAsnTyrGlyValLeuGlyMetMetCysIleHisTrpLysGlyProLeuArgLeuGln
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different forms of wild type human presentlin-1 (PS-1). The form
celliferent forms of wild type human presentlin-1 (PS-1). The form
represented by this sequence results from alternate splicing of the
genomic DNA. AAT40031 represents the coding sequence for wild type human
PS-2. The presentlins are a family of highly conserved integral membrane
proteins with a common mutational hot spot regions. Mutations in PS genes
are implicated in familial Alzheimer's disease (AD) and possibly other
diseases such as cerebral haemorrhage, schizophrenia, depression etc., so
detection of mutations in these sequences can be used for diagnosis of
these diseases. The encoded proteins, or vectors that express them or
containing antisense sequences, antibodies selective for mutant forms of
the encoded proteins (such as AAW05736) and modulators of PS gene
containing are useful as models for drug screening. The antibodies can also
be used e.g. for affinity purification and in immunoassays.
                                                                                                                                                Presentlin-1, human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New presentin genes - useful for diagnosis, therapy and drug
screening of familial Alzheimer's disease, cerebral disorders,
                                                                                                                    Presenilin-1-2, alternatively spliced coding sequence.
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Matches:
Conservative:
Mismatches:
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547..1948
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28-JUN-1995;
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AAT40029
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17 Gaps: 18. AAT40029 (1-3086) ASPGIUASNVAIVAIGIUGIUAIAGIULEUI	o,	ystyrdlyalaserHisValile 51	alValPheThrMetAsnThrIle 71	SerHisProPheValargGluThr 91	Instruction Instruction	ysTyrLysPheTyrLysLeuIle 131	heLeuPheThrThrIleTyrVal 151	NaLeuleuValLeuPheGlyLeu 171 ::: ::: NCATTACTGTTGCACTCCTGATC 1150	rpLysGlyProLeuArgLeuGln 191	euValPheIleLysTyrLeuPro 211	AlTrpAspLeuValAlaValLeu 231	AlaGinGluArgAsnGluProlle 251	ProTyrValLeuValThrAlaVal 271		rgProLysValLysArgllePro 311	Arg 331 AGT 155	argGluLeuAlaAlaGlu 339	iisArgHisGludludludludrg 356 ::: SCTGGTGAAGACCCAGAGGAAAGG 1675
1.7 1.7 1.7 1.0 1.461) x AAT4002 1.5 1.6	Gaps (1-3086)	alGluGluAlaGluLeuLy ArGAGGAGCTGACATTGAR	erLeuCysMetAlaLeuVa :: crcrcrGCATGGTGGTGGT	snGlyArgHisLeuLeuSe :: ::: ATGGGCAGCTAATCTP	lyLeuMetSerLeuGlyAs 	euleullevalPheTyriy ::: ccrggrggrrcrgrara	erSerPheLeuLeuLeuBl ATCTCTATTGTTGCTGTT	heAspValSerProSerAl ::::: ::: ATAACGTTGCTGTGGACTA		etSeralaLeuMetAlaLe ::	alleuphevalileserva :: TCTTGGCTGTGATTTCAGT	rgTyrLeuValGluThra] 	erSerGlyVallleTyrP; CCTCAACATGGTGTGG-	rgGluProThrSerSerAs :: : AAAGGAGAGTATCCAAAA	erSerGluThrProLysAl ::::: ::: prGCaGaAaGCaCaGaaa	erasnthrThralaserTè 	GGGACAGTCATCTAGGGC	laAsnPheHi i:: TTTCCAGCAGTATCCTCG(
O-8 O C 1 O 1 A O-0 H-A H O-0 O H O O O O-0 H A O A O O O O H A O O O O O O O O O O	17 (1-461) x AAT4002	ilngluaspgluasnvalv. ::::: :agcaagatgaggaagag	listeuPhevalProvalSe .rgctctrrgtcccrgtGA	hrPheTyrSerGlnAsnAl :: :::::: :GCTTTTATACCCGGAAGG	spSerlleValGluLysG	alvalLeuMetThrvalL :: ::: ::: TGTTGATGACTATCC	iisGlyttpLeullevalS 	:InGluValLeuLysSerP :GGGAAGTGTTTAAAACCT	ilyAsnTyrGlyvalLeuG ::: GGAATTGGGTGTGGTGG	llapheTyrLeulleThrM 	iluTrpThrvalTrpPheV AATGGACTGCGTGGCTCAV	thrProlysglyProleua	PheProblateulleTyrs TTCCAGCTCTCATTTACT	iluasnThrThraspProa aaGGaGaCCCGGaaGCTC	og1	nLysV	Valglu GAGGAATGGGAAGCCCAGA	ArgProThrValGlnAspA GAGCTGCTGTCCAGGAAC

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377 SerTyrPhe-----AspTrpAsnThrThrIleAlaCysTyrValAlaIleLeuIleGly 394
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1736 GCAACAGCAGTGGAACTGGAACACAACCATAGCCTGTTTCGTAGCCATATTAATTGGT 1795
414 eProPheSerProAspSerPhePheThrPheValProAlaGlySerSerProHisLeuLe 434
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Sequence 14, Appl
Sequence 8, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 28131, A
Sequence 4373, Ap
                                             Sequence 290, App
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                                                                Sequence 5, Appli
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Sequence 29,
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Sequence 8,
Sequence 7,
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Sequence 3
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ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
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US-09-938 842A-1045
US-10-180-781-14
US-09-895-035-8
US-09-895-035-3
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US-10-029-386-18073

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US-09-818-875-4212
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              US-09-785-474-27

US-10-293-000-7

US-10-116-275-290

US-10-221-254-5
                                                                               US-09-785-474-31
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US-09-895-035-13
US-09-754-949-3
US-10-417-422-3
US-10-417-422-3
US-09-878-454A-25
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US-10-221-254-7
US-09-754-949-5
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WASCO, WILMA
                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 32
US-09-785-474-1
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33.44.5
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708.031 Million cell updates/sec
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                                                                                                                   December 11, 2003, 07:41:57; Search time 2164 Seconds
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| cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                    protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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975 GAATGGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTG 1034
                                                                                                  .035 IGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAAAATGAAAACGCTT 1094
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                                                                                                                                                 PheProAlaLeuIleTyrSerSerGlyValIleTyrProTyrValLeuValThrAlaVal 271
                                                                                                                                                                                                                                                                                  ProGlyGluAlaSerCysSerSerGluThrProLysArgProLysVallysArgllePro 311
                                                                                                                                                                                                                                                                                                                                               312 GlnLysValGlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg 331
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                                                                             232 ThrProLysGlyProLeuArgTyrLeuValGluThrAlaGlnGluArgAsnGluProlle
                                                                                                                                                                     CGAGCTGCTGTCCAGGAACTTTCCAGCAGTATCCTCGCTGAAGAACCCCAGAGGAAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                           ---ArgGluLeuAlaAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 ArgProThrValGlnAspAlaAsn ... ---- PheHisArgHisGluGluGluGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerTyrPhe-----AspTrpAsnThrThrIleAlaCysTyrValAlaIleLeuIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 GluTrpThrValTrpPheValLeuPheValIleSerValTrpAspLeuValAlaValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Genetic Alterations Related To Familial Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON STATE: DC COUNTRY: USA ZIP: 20005-3934
                                                                                                                                                                                                                                                  1146 GAAGGAGACCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/09785474
Patent No. US20010012626A1
GENERAL INFORMATION:
APPLICANT: INAIL, RUDOLPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGACTGTGGGCCCAGAGAGCCCTGCACTCTAATTCTGAATGCTGCCATCATGATGTGC 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       675 AITGITGICAIGACIAICCICCIGGIGGTICIGIAIAAAAAAGIGGGGCGAIAAAGGICAIC 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValValLeuMetThrValLeuLeuIleValPheTyrLysTyrLysPheTyrLysLeuIle 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisGlyTrpLeulleValSerSerPheLeuLeuLeuPheLeuPheThrThr1leTyrVal 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyAsnTyrGlyValLeuGlyMetMetCyslleHisTrpLysGlyProLeuArgLeuGln 191
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215
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48
FILING DATE: 20-Feb-2001
CLASSIPICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REFERENCE/DOCKET NUMBER: 0609.4180002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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TELEPX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 249..1649
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                         LENGTH: 2765 base pairs
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.17e-98
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65.17%
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                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                          FEATURE
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APPLICANT: Monteiro, Mervyn J.
APPLICANT: Mah, Alex L.
APPLICANT: Perry, George
APPLICANT: Smith, Mark A.
TITLE OF INVENTION: UBIQUILIN, A PRESENILIN INTERACTOR AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                   ::: ||||||||
200 GAAAGCACAGAAAGGGAGTCACAAAGACACTGTTGCAGAAATGATGATGAGGGGGTTCAGT 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1260 GAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTCA 1319
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                                                                                                                                                                                       ThrProLysGlyBroLeuArgTyrLeuValGluThrAlaGlnGluArgAsnGluProlle 251
                                                                                                                                                                                                                          cerccaaaagerccacrrcerargergerraaaacagercaggagaaargaaacgerr 1094
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                                                                                                                                                                                                                                                              PheProAlaLeu11eTyrSerSerGlyVal11eTyrProTyrValLeuValThrAlaVal 271
                                                                                                                                                                                                                                                                                                                                                                                                     ProGlyGluAlaSerCysSerSerGluThrProLysArgProLysValLysArgIlePro 311
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GGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTAAAGCCTCA
                                                                                                                       GluTrpThrValTrpPheValLeuPheValIleSerValTrpAspLeuValAlaValLeu
                                                                                                                                                                                                                                                                                                                                  GluAsnThrAspProArgGluProThrSerSerAspSerAsnThrSerThrAlaPhe
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                                                      GlnPheTyrLeuIleThrMetSerAlaLeuMetAlaLeuValPheIleLysTyrLeuPro
                                                                      312 GlnLysValGlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg
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; Publication No. US20030175278A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 GlnGluAspGluAsnValValGluGluAlaGluLeuLysTyrGlyAlaSerHisValIle
                              COMPUTER: ISEN FOR COMPATIBLE
COMPUTER: ISEN FOR COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
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Matches:
Conservative:
Mismatches:
Indels:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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LOCATION: 249..1649
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
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INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 2765 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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   COMPUTER READABLE FORM:
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Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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GENERAL INFORMATION:
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APPLICANT: Blan Pharmaceutical Technology
APPLICANT: Blan Pharmaceutical Technology
APPLICANT: Brayden, David
APPLICANT: Barden, David
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Inselda
APPLICANT
                                                                                                                                                                                                                                                                                                                                                                      1260 GAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTCA 1319
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                                                ProGlyGluAlaSerCysSerSerGluThrProLysArgProLysValLysArgIlePro
                                                                                                                              312 GlnLysValGlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg
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1440 GCAACAGCCAGTGGAAGACTGGAACACATAGCCTTTCGTTTCGTAGCCATATTAATTGGT
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          1146 GAAGGAGCCCGGAAGCTCAAAGGAGAGTATCCAAAATTCC-
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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FILE REFERENCE: 4115-175
CURRENT APPLICATION NUMBER: US/10/293,000
CURRENT FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: US 60/338,549
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/10221254; Publication No. US20030113811A1; GENERAL INFORMATION: APPLICANT: GLAXO GROUP LIMITED 7 TITLE OF INVENTION: ASSAY; FILE REFERENCE: PG3950USW; CURRENT APPLICATION NUMBER: US/10/221,254; CURRENT FILING DATE: 2002-09-10; PRIOR PPLICATION NUMBER: 0005894.1; PRIOR FILING DATE: 2000-03-10; NUMBER OF SEQ ID NOS: 7
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US-09-785-474-31
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|TIGIGCCTIACATIATIACICCTIGCCAITITICAAGAAAGCAITGCCAGCICTICCAAIC 1559
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                                                        GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171
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|GGGGAAGTGTTTAAAACCTATAACGTTGCTGGGACTACATTACTGTTGCACTCCTGATC 854
                                                                                                                                                                                           GlyAsnTyrGlyValLeuGlyMetMetCysIleHisTrpLysGlyProLeuArgLeuGln 191
                                                                                                                                                                                                                                                                   GlnPheTyrLeuIleThrMetSerAlaLeuMetAlaLeuValPheIleLysTyrLeuPro 211
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ATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATC 734
                                    HisGlyTrpLeuIleValSerSerPheLeuLeuLeuPheLeuPheThrThrIleTyrVal 151
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ADDRESSE: STERNE, KESSLER, GOLDSTEIN & POX STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
CUUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PLAN PC COMPATIBLE
COMPUTER: PLAN PC COMPATIBLE
COMPUTER: PLAN PC COMPATIBLE
COMPUTER: PLAN PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: VUNKNOWN>
                                                                                                      TITLE OF INVENTION: Genetic Alterations Related Alzheimer's Disease
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Matches:
Conservative:
Mismatches:
Indels:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-195
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 249..1649
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 40,679
Sequence 31, Application US/09785474
Patent No. US20010012626A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2765 base pairs
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                             APPLICANT: TANZI, RUDOLPH
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434 uHisLysSerLeuLysSerValTyrTyrIleAsnSerLeuPhe-----LeuProPh 451
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Matches:
Conservative:
Mismatches:
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REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609.4180002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Peb-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
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SEQUENCE DESCRIPTION: SEQ ID NO: 29:
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FILING DATE: 30-AUG-1996
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FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                               Sequence 29, Application US/09785474
Patent No. US20010012626A1
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
WASCO, WILMA
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SEQUENCE CHARACTERISTICS:
LENGTH: 2765 base pairs
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STRANDEDNESS: double
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                                                                                     1677 GATGTTTCTT 1689
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 32
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Best Local Similarity:
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                                                                                                                                   RESULT 7
US-09-785-474-29
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                                                                                    112 ValvalbeuMerThrValbeuleuleValPheTyrLysTyrLysPheTyrLygLeulle 131
                                                                                                     132 HisGlyTrpLeuIleValSerSerPheLeuLeuPheUPheThrThrIleTyrVal 151
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TITLE OF INVENTION: Genetic Alterations Related To Familial Alzheimer's Disease
                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 2005-3934
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
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uHisLysSerLeuLysSerValTyrTyrIleAsnSerLeuPhe-----LeuProPh 451
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vez
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Peb-2001
CLASSIFICATION: UNKNOWN:
APPLICATION NUMBER: 08/706,344
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, UUDITH U.
REGISTRATION NUMBER: 40,679
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09785474 Patent No. US20010012626A1 GENERAL INFORMATION:
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979.50
64.72%
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US-09-785-474-3
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AGCTITTATACCCGGAAGGATGGGCAG---CTAATCTATACCCCATTCACAGAAGATACC 614
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1200 GAAAGCACAGAAAGGGAGTCACAAGACACTGTTGCAGAGAATGATGATGATGGCGGGTTCAGT
                                                                                                                                    AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal
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                                                                ThrPheTyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr
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ORGANISM: Homo sapiens
FEATURE:
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SEQ 1D NO 13
LENGTH: 1392
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Best Local Similarity:
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Pred. No.:
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US-09-895-035-13
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                                                           138 GAGCAAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCCAAGCATGTGATC 497
                                                                                                                                                                                                                      92 AspSerIleValGluLySGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal 111
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                                                                                         52 HisLeuPheValProValSerLeuCysMetAlaLeuValValPheThrMetAsnThrIle 71
                           32 GlnGluAspGluAsnValValGluGluAlaGluLeuLyaTyrGlyAlaSerHisValIle
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US-09-043-944-1 (1-461) x US-09-785-474-3 (1-2765)
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377 SerTyrPhe-----AspTrpAsnThrThrIleAlaCysTyrValAlaIleLeuIleGly 394
                                                                                                                                                                                       LeuCysPheThrLeuValLeuLeuAlaValPheLysArgAlaLeuProAlaLeu-GlnPh 414
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; OTHER INFORMATION: Incyte ID No. US20020082211A1 g1244637
US-09-895-035-13
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APPLICANT: Murry, Lynn E.
APPLICANT: Maser, Matthew R.
TITLE OF INVENTION: HUMAN PRESENILIN VARIANT
FILE REFERENCE: PC-0047 CIP
CURRENT APPLICATION NUMBER: US/09/895,035
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/116,640
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ. ID NOS: 14
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ORGANISM: HOMO
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                                                                                                               TYPE: DNA
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                                     GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171
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ThrProLysGlyProLeuArgTyrLeuValGluThrAlaGlnGluArgAsnGluProlle
                            HisGlyTrpLeuIleValSerSerPheLeuLeuPheLeuPheLeuPheThrThrIleTyrVal
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|GGGGAAGTGTTTAAAACCTATAAGGTTGCTGTGGACTACATTACTGTTGCACTCCTGATC
                                                                                                                                              GluTrpThrValTrpPheValLeuPheValIleSerValTrpAspLeuValAlaValLeu
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GCAACAGCCAGTGGAAACTGGAACACAAACCTGTTTTCGTAGCCATATTAATTGGT
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| Patent No. US2002015939A1
| GENERAL INFORMATION:
| APPLICANT: CORDELL, BARBARA
| TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS OF
| TITLE OF INVENTION: NEURONAL DEGENERATION
| FILE REFERENCE: SCIOS.012A
| CURRENT APPLICATION NUMBER: US/09/754,949
| CURRENT FILING DATE: 2001-01-04
| NUMBER OF SEQ ID NOS: 16
| SOFTWARE: FastSEQ for Windows Version 4.0
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213
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103
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Matches:
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Best Local Similarity: 49.31* Mismatches: 103 Query Match: 41.77* Indels: 45 DB: 13	4)	Oy 32 GInGluAspGluAsnValValGluGluAlaGluLeuLysTyrGlyAlaSerHisValIle 51	170 GROCHMAN GOVERNAM CANGAROCI CANGAR AND AND AND AND AND AND AND AND AND AND	250 ATGCTCTTTGTCCCTGTGACCTTCTGCATGGTGGTGGTGGTGGTCGTATAAGTCAGTC	Qy 72 ThrPheTyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr 91	DD 310 AGCTTTATACCCGGAAGGATGGCCAGCTAATCTATACCCCATTCACAGAAGATACC 366	Qy 92 AspSerIleValGluLySGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal 111	Db 367 GAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATGTGTC 426 Ov 112 ValvalLeumetThrValleuleullevalPheTvrlvsTbrlvsPheTvrlvsBheTvrlvsIeuIle 131	427 AITGITGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATC	Oy 132 HisGlyTrpLeuIleValSerSerPheLeuLeuPheLeuPheThrThrIleTyrVal 151	487 CATGCCTGGTTATTATATCATCTCTATTGTTGTTGTTGTTTTTTTT	Db 547 GGGAAGTGTTTAAAACCTATGCGTGGAGACTATAATTACTGATGACTATGATGATGATGATGATGATGATGATGATGATGATGATG	172 GlyAsnTyrGlyValLeuGlyMetMetCysIleHisTrpLysGlyProLeuArgLeuGln	:::	Qy 192 GlnPheTyrLeuIleThrMetSerAlaLeuMetAlaLeuValPheIleLysTyrLeuPro 211	Db 667 CAGGCATATCTCATTAGGTGCCCTCATGGCCCTGGTGTTATCAAGTACCTCCT 726	Qy 212 GluTrpThrValTrpPheValLeuPheValIleSerValTrpAspLeuValAlaValLeu 231	Db 727 GAAIGGACTGCGIGGCTCATCTIGGCTGTGATTTCAGTATATAGTGGCTGTTTTG 786	Qy 232 ThrProLysGlyProLeuArgTyrLeuValGluThrAlaGlnGluArgAsnGluProlle 251	787 IGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACACCTCAGGAGAAATGAAACGCTT	252 PheProAlaLeulleTyrSerSerGlyValIleTyrProTyrValLeuValThrAlaVal	847 ITTCCAGCTCTCATTTACTCCTCAAAAGGTGGGTTGGTGAATATGGCA	OY 2/2 GLUASNIDETHERAPPERANGGIUPFORINESESSERASDISETASNIDESETHERAPHS 291	UY 294 FIOGLYGIUALASSEKCYSSGESEGTOLINIKFIOLYSBAGGENDSBALLYSBAGGILEFFO 311 Dh 040	The state of the s	312 GlnLysValGlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg	967GAGTCACAAGACACTGTTGCAGAGAATGATGGGGGGTTCAGT	332 ValGluArgGluLeuAlaAlaGlu	1012 GAGGAATGGGAAGCCCAGAGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTCA	340 ArgProThrValGlnAspAlaAsnPheHisArgHisGluGluGluBurg	DD 1072 CGAGCTGCTGTCCAGGAACTTTCCAGCAGTATCCTCGCTGGTGAAGACCCAGAGGAAGG 1131
Qy 252 PheProAlaLeuIleTyrSerSerGlyValIleTyrProTyrValLeuValThrAlaVal 271	Qy 272 GluAsnThrThrAspProArgGluProThrSerSerAspSerAsnThrSerThrAlaPhe 291	Db 898 GAAGGAGACCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCC939	040	312 GlnLysValGlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg	Db 967GAGTCACAAGACACTGTTGCAGAAATGATGATGGTGGCGGGTTCAGT 1011	Qy 332 ValGluQy 332 ValGluQy 339 (1)	Db 1012 GAGGAÁTGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTCA 1071	Qy 340 ArgProThrValGlnAspAlaAsnPheHisArgHisGluGluGluGluLuArg 356	GlyValLysLeuGlyLeuGlyAspPhellePheTyrSerValLeuLeuGlyLysAlaSer	Db 1132 GGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTGGT	Qy 377 SerTyrpheAspTrpAsnThrThrIleAlaCysTyrValAla1leLeuileGly 394 nh 1192 Granden Common	395 LeuCyspheThrLeuValLeuLeuAlaValPheLysArgAlaLeuProAlaLeu-GlnPh 41	1252 TIGIGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATC	Qy 414 eProPheSerProAspSerPhePheThrPheValProAlaGlySerSerProHisLeuLe 434	1312 TCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTACAC	Qy 434 uHisLysSerLeuLysSerValTyrTyrIleAsn 445	Db 1369 ATGGACCAATTAGCATTCCATCAATTTTÄTÄTCT 1402	RESULT 11 US-10-417-422-3	; Sequence 3, Application US/10417422 ; Publication No. US20030219720A1	~	APPLICANT: CORDELL, BAKBARA APPLICANT: SCIOS, INC. ATTER OF INITIATION MEMBERS BOD IDENMITEDIAN INITIATION		CURRENT APPLICATION NUMBER: US/10/417,422 ; CURRENT FILING DATE: 2003-04-14			SOCIAME: FASCED LOI WINDOWS VELSION & SEQ ID NO 3 3 1 ENVIRON 110A	TYPE: DAY	; OKGANISM: HOMO SAPIEN US-10-417-422-3		Pred. No.: 5.19e-97 Length: 1404 Score 50079.00 Matches 213 Percent Similarity. 65 74* Conservative. 71	

Alignment Scores: Pred. No.: Pred. No.: Score 5 Length: 2285 Score 60 Percent Similarity: 61.95\$ Conservative: 60 Best Local Similarity: 48.67\$ Mismatches: 94 Overy Match: 9 Gaps: 12 US-09-043-944-1 (1-461) x US-09-878-454A-25 (1-2285)	Qy 2 ProSerThrArgArgGlnGlnGluGlyGlyGlyAlaAspAlaGluThrHisThr 19	Qy 20 ValTyrGlyThrAsnLeuIleThrAsnArgAsnSerGlnGluAspGluAsn 36 bb 498 GCCCAGTGCAGAAACCAGAGAAGAGAGGACGGTGAGGACCCTGACCGTATGTC 557		618 GCGAAGCATGTGTTTTTTTTTTTTTTTTTTTTTTTTTTT	VY 67 ThrmetAshThrileThrPheTyrSerGlnAshGAyArgHisLeuLeuSerHisPro 86	Oy 87 PheValArgGluThrAspSexIleValGluLy8GlyLeuMetSerLeuGlyAsnAlaLeu 106	Qy 107 ValMetLeuCysValValValLeumerThrValLeuLeulleValPheTyrLysTyrLys 126 :::	Qy 127 PheTyrLysLeulleHisGlyTrpLeulleValSerSerPheLeuLeuLeuPheLeuPhe 146	Qy 147 ThrThrIleTyrValGluValLeuLysSerPheAspValSerProSerAlaLeuLeu 166	Qy 167 ValLeuPheGlyLeuGlyAsnTyrGlyValLeuGlyMetMetCysIleHisTrpLysGly 186 :::	QY 187 ProLeukrgLeuGlnGlnPheTyrLeulleThrMetSeralaLeuMetalaLeuValPhe 206	Qy 207 IleLysTyrLeuProGluTrpThrValTrpPheValLeuPheValIleSerValTrpAsp 226	Qy 227 LeuValalaYalLeuThrProLysGlyProLeuArgTyrLeuValGluThralaGlnGlu 246	Qy 247 ArgAsnGluProllePheProAlaLeulleTyrSerSerGlyVal11eTyrProTyrVal 266	7 LeuValThr AlaValGluAsnThrAspProArg 278	279
Oy 357 GlyValLysLeuGlyLeuGlyAspPhellePheTyrSerValLeuLeuGlyLysAlaSer 376	eProPheSerProAspSerPhePheThrPheValProAladlySerSerProHisteule 434	434 uHisLysSerLeuLysSerValTyrTyrIleAsn 445	RESULT 12 US-09-878-454A-25 ; Sequence 25, Application US/09878454A ; Patent No. US20020064828A1	; GENERAL INFORMATION: ; APPLICANT: Monteiro, et al. ; TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentlin; FILE REPERENCE: 4115-161	CURRENT APPLICATION NUMBER: US/09/878,454A; CURRENT FILING DATE: 2001-06-11; PRIOR APPLICATION NUMBER: 60/210,939	; PRIOR FILING DATE: 2000-06-11 ; NUMBER OF SEQ ID NOS: 26 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 25) I.BNGTH: 2285 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE:	NAME/KBY: misc feature : LOCATION: (2137)(2137) : OTHER INFORMATION: n can be a, c, t or g : NAME/KEY: misc_feature	; LOCATION: (2144)(2144) ; OTHER INFORMATION: n can be a, c, t or g ; NAME/KBY: misc feature ; LOCATION: (2152)(2152)	COTER INFORMATION: n can be a, c, t or g NAME/KEY: misc feature LOCATION: (2157)(2157) OTHER INFORMATION: n can be a, c, t or g	; NAME/KEY: misc feature ; LOCATION: (2160)(2160) ; OTHER INFORMATION: n can be a, c, t or g ; NAME/KEY: misc_feature	; LOCATION: (2163)(2163) ; OTHER INPORMATION: n can be a, c, t or g ; NAME/KEY: misc feature ; LOCATION: (2180)(2180)	CTHER INFORMATION: n can be a, c, t or g NAME/KEY: misc feature LOCATION: (2203)(2203) OTHER INFORMATION: n can be a, c, t or q	be a, c, t or	(2216 ORMATI misc	: LOCATION: (2225) ; OTHER INFORMATION: n can be a, c, t or g

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1566 CTGACCTCCTGCTGCTTGCTGTGTTCAAGAAGGCGCTGCCGCCCTCCCCATCTCCATC 1625
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                                                                                 1365 ------ccrrcataccccaagrcrrrgagccrccc------- 1394
                                                                                                                                                                                                                                                                                             LysLeuGlyLeuGlyLeuGlyAspPhellePheTyrSerValLeuLeuGlyLysAlaSerSer--- 377
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                                        299 SerGluThrProLysArgProLysValLysArgIleProGlnLysValGlnIleGluSer 318
                                                                                                                            319 AsnThrThrAlaSerThrThrGlnAsnSerGlyValArgValGluArgGluLeuAlaAla 338
                                                                                                                                                                                                              339 GluargProThrValGlnAspAlaAsnPheHisArgHisGluGluGluGluArgGlyVal 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group FLLC
STREET: 701 Fifth Ave, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                       -----TTGACTGGCTACCCAGGGGAGGAGCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1626 ACGITCGGCCTCATCTTTACTTCTCCACGGACAAC 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PheProPheSerProAspSer 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 920010.571C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/180,781
FILING DATE: 24-Jun-2002
CLASSIFICATION: <UNKNOWN>
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Schellenberg, Gerard
Wasco, Wilma
Levy-Lahad, Ephrat
Bird, Thomas D.
Galas, David J.
1335 GAAGAAGACTCCTATGACAGTTTT--
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SEQUENCE CHARACTERISTICS:
LENGTH: 2236 base pair
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10180781
Publication No. US20030180880A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
STATE: Washington
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US-10-180-781-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 ilelysTyrLeuProGluTrpThrValTrpPheValLeuPheValIleSerValTrpAsp 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500 GCCCAGTGGAGAAAGCCAGGAGAAGGAGGACGATGAGGAGGAGGACCCTGACGCTATGTC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 ValmetLeuCysValValValLeumetThrValLeuLeulleValPheTyrLysTyrLys 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 ThrThrileTyrValGInGluValLeuLysSerPheAspValSerProSerAlaLeuLeu 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   620 GCGAAGCACGTGATCATGCTGTTTTGTGCCTGTCACTCTGTGCATGATCGTGGTGGTAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 ValTyrGlyThrAsnLeuIleThrAsnArgAsnSerGlnGluAspGluAsn-----
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219
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Mismatches:
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                                                                                                                                                             Length:
Matches:
                           SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                               1.06e-94
961.00
61.73$
48.45$
TOPOLOGY: linear
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37	Qy 67 ThM6tAsnThx1leThrPheTyrSerGlnAsnAsnGlyArgHisteuLeuSerHisPro 86	OY 107 ValMetLeuCysValValValLeuMetThrValLeuLeuLleValPheTyrLysTyrLys 126	147 917 167	Db 977 CICTIGCTGACTGTCGGGCAGTGGGGATGGTGTGCATCCACTGGAAGGGC 1036	246 121 266 127 278	279 GlubrofhrSerSerAspSerAsnThrSerThrAlaPheProGlyGludlaSerCysSer 29 GlubrofhrSerSerAspSerAsnThrSerThrAlaPheProGlyGludlaSerCysSer 29	319 ASNThrThr 1397 339 GluArgPro 1427 359 LysLeuGly 1448 AAGCTTGGC
Oy 279 GluProThrSerSerAspSerAsnThrSerThrAlaPheProGlyGluAlaSerCysSer 298	1397TTGACTGGCTACCCAGGGGAGGAGCTGGAGCTGGAGCTGGAGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGAGAGAGA	Cy 359 LysLeuGlyLeuGlyAspPhellePheTyrSerValLeuLeuGlyLysAlasSerSer 377		RESULT 14 US-10-293-000-8 Sequence 8, Application US/10293000 Publication No. US2030175278A1 GENERAL INFORMATION: APPLICANT: Mah, Alex L. APPLICANT: Perry, George	APPLICANT: Smith, Mark A. TITLE OF INVENTION: UBLOUILIN, A PRESENILIN INTERACTOR AND METHODS OF USING SAME FILE REPERENCE: 4115-175 CURRENT APPLICATION NUMBER: US/10/293,000 CURRENT FILING DATE: 2003-04-01 PRIOR PPLING DATE: 2001-11-13 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin version 3.2 SEQ ID NO 8 LENGTH: 2236	Homo sapiens ss: 1.76e-94 Length: 959.00 Matches: ity; 61.73% Conservati	48.45 Mismatches: 40.33

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Search completed: December 11, 2003, 10:18:31
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                                               397 PheThrLeuValLeuLeuAlaValPheLysArgAlaLeuProAlaLeuGln-----
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                                                                                                                                                            Sequence 7, Application US/10221254
) Publication No. US20030113811A1
) GENERAL INFORMATION:
| APPLICANT: GLAXO GROUP LIMITED
| TITLE OF INVENTION: ASSAY
| FILE REFERENCE: PG3950USW
| CURRENT APPLICATION UNDHER: US/10/221,254
| CURRENT FILING DATE: 2000-09-10
| PRIOR APPLICATION NUMBER: 0005894.1
| PRIOR FILING DATE: 2000-03-10
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: PATENTIN VET: 2.1
| SEQ ID NO 7
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; LOCATION: (368)..(1714)
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 AsnThrThrAlaSerThrThrGlnAsnSerGlyValArgValGluArgGluLeuAlaAla 338
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                                                                                                          147 ThrThrileTyrValGlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeu 166
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127 PheTyrLysLeuIleHisGlyTrpLeuIleValSerSerPheLeuLeuLeuPheLeuPhe
                             857 TGCTACAAGTTCATCCATGGCTGGTTGATCATGTCTTCACTGATGCTGCTGTTCCTCTTC
                                                                                                                                                                                                                                                     167 ValleuPheGlyLeuGlyAsnTyrGlyValLeuGlyMetMetCysIleHisTrpLysGly
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

December 11, 2003, 06:24:06; Search time 93 Seconds (without alignments) 2187.931 Million cell updates/sec Run on:

US-09-043-944-1

2378 1 MPSTRRQQEGGGADAETHTV.......YXINSLFLPFLCIINFSIIS Perfect score: Sequence: Title:

BLOSUM62 Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

Total number of hits satisfying chosen parameters: 569978 segs, 220691566 residues Searched:

1139956

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
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-MODEL=frame+ p2n.model - DEV=xlp
-0=/con2 1/USFT0_spool_p/US09043944/runat_11122003_062401_3701/app_query.fasta_1.647
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-NOSMPAD - LARGEGUERY - NEG_SCORES=0 - WAIT - DSPBLOCK=100 - LONGLOG
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Database :

Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		* Query				
No.	Score	Match	Match Length DB	B	QI.	Description
-	2052.5	86.3	4137	4	US-08-832-867-1	Sequence 1, Appli
7	994.5	41.8	2765	m	US-08-706-344C-1	Sequence 1, Appli
m	994.5	41.8	2765	m	US-08-706-344C-27	27.
4	993.5	41.8	1488	N	US-08-875-972-3	<u>س</u>
Ŋ	993.5	41.8	2764	m	US-08-923-454A-9	Sequence 9, Appli
9	993.5	41.8	2764	4	US-08-832-867-2	
7	993.5	41.8	2765	m	US-08-888-077A-1	, -i
8	993.5		2791	ď	US-08-967-101-133	133
σ	993.5	41.8	2791	N	US-08-592-541-133	
10	993.5	41.8	2791	m	US-09-124-698-133	133,
11	993.5	41.8	2791	m	US-09-127-480-133	Sequence 133. App
12	993.5	41.8	2791	4	US-09-124-523-133	Sequence 133, App

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09-636-796A-13	08-496-84	08-670-9	-96	08-706-344	-08-967-1	-595-	09-124-6	09-127-4	08-496-	-124-5	09-636-7	08-431-	08-888-07	5	08-592-541-	-60-	-09-127	\sim	-09-124	-09-636	18-431-	08-967-101-13	8-592-541-13	-09-124-698	7-480-13	-124-523-	-09-636-796A-1	-08-888-077A-1	-08-496-841	-09-544-618-1	-08-967-101-1	US-08-592-541-165
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ALIGNMENTS

SULT 1 -08-832-867-1 Sequence 1, Application US/08832867C Sequence 1, Application US/08832867C Sequence 1, Application US/08832867C GENERAL INFORMATION: APPLICANT: BAUMEISTER, Ralf TITLE OF INVENTION: CONFERRING EXPRESSION OF A HETEROLOGOUS DNA SEQUENCE IN TITLE OF INVENTION: ELEGANE CELLS AT ALL STAGES OF DEVELOPMENT IN C. TITLE OF INVENTION: ELEGANS AND USES THEREOF FILE REPREBACE: 674503-2004	CURRENT APPLICATION NUMBER: US/08/832,867C CURRENT FILING DATE: 1997-04-04 CURRENT FILING DATE: 1997-04-04 SOFTWARE: Patentin Ver. 2.0 EQ ID NO 1 LENGTH: 4137 TYPE: DNA ORGANISM: Caenorhabditis elegans	Alignment Scores: 2.38e-226 Length: 4137 Pred. No.: 2082.50 Matches: 459 Score: Sanilarity: 58.82\$ Conservative: 1 Best Local Similarity: 58.70\$ Mismatches: 1 Query Match: 4 Gaps: 7	US-09-043-944-1 (1-461) x US-08-832-867-1 (1-4137) QY
RESULT 1 US-08-832-867-1 Sequence 1, A Sequence 1, C GENERAL INFOR TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV TITLE OF INV FILE REFERENCE	CURRENT APPL CURRENT FILI NUMBER OF SE SOFTWARE: Pa SEQ ID NO 1 TYPE: DNA TYPE: DNA ORGANISM: C	Alignment Scores: Pred. No.: Score: Percent Similarit Best Local Simila Query Match: DB:	US-09-043-94 Qy Db 96

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ð í	37 IValGluGluAlaGluLeuLySTYrGlyAlaSerHisVallleHisLeuPheValProVa 57	à 8	261 ValileTyrProTyrValleuValThrAlaValGluAshThrThrAspFroArgGlu
a &		\$ 6	281 ThrSerSerAspSerAsn
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ر ال	77 nAsnGlyArgHisLeu	ପ୍	2340 AATTTCAGCTTCTACAGCTTTTCCTGGAGAGGCGAGTTGTTCATCTGAAACGCCAAA
3 8		ð í	304 gProlysValLysArglleProGlnLysValGlnlleGluSerAsnThrThrAlaSe
qq	1320 TIAICAATTIGCAICIGIGCAATCGCACTCTITGICAGIGCAAAATAATTTTIGGICAGT 1379	g ä	
λ	84 84	<u>₹</u> 8	5.4 TINGSINASIDELGAYVAIAEGVALGAUAEGGAUGUAEGAAGAUAEGAGAGAGAGAGAGAGAGAG
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à i		q	2520 AGACGCCAATTTTCACAGGCACGAAGAGGAAGAGAG-TGAGTGAAAAACGTGCTGAA
වූ	TTAACTATTTTGGTGGTTTTTAATTTTTACTCAATTTTCTATCAATATTTGTTTG	ò	356
8 8	**************************************	qq	2579 GGGCAAAAGGGGGATGTATTTTCGCAAATTTTACTCGAACTTTCTCACTTCTAACTCA
a a	GITGAAGAITTACICTGGAAATTICGAAATAAACTGTAAATGGAAAAATGGAACACACACA	ò	356
ð 5	85	qa	2639 GTTTTTTCTTGACAGCACAAAACGAAAATATTGCCGTCTACGTTCGGTATCGAAATA
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7 원	0 TIGICAGCAGITITICITICITICITITICCAATCAATCAATGIGCAGTAAGTIGATA	qa	2819 AGAITCAAGAAAGAICICAAAIAAACITGCAAGCITGCCACITGCGCIAGTCACGAA
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<u>ک</u> او	181 ysileHisTrpLysGlyProLeuArgLeuGlnGlnPheTyrLeulleThrMetSerAlaL 201 1920 GTATARGARAGATGCARTGAGTGARGAGTTCARATACARATGARA 1939	qQ	
à	euMetAlaLeuValPheileLysTyrLeuProGluTrpThrValTrpPheValLeuPheV	λö	383 ThrileAlaCysTyrValAlaIleLeuileGlyLeuCy9PheThrLeuValLeuLe
<u> </u>	TAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGGTTTGTGCTGTTTG	q	3059 GACTATGGCTTGTTATGTGGCCATTCTTATCGGTCTCTGCTTCACTTGTCCTGCT
λ	221 allieSerValTrpAspLeuValAlaValLeuThrProLysGlyProLeuArgTyrLeuV 241	දු ද	403 aValPheLysArgAlaLeuProAlaLeu-GlnPheProPheSerProAspSerPheP 3119 (GT/(TIPLE)
අධ	2040 TIATCICGGITIGGGAICIGGITGCCGIGCTCACACCAAAAGAACCATIGAATATIGG 2099	3 8	
ζŏ	241 alGluThrAlaGlnGluArgAsnGluProIlePheProAlaLeuIleTyrSer 258	3 A	3179 CTTTTGTACCCGCTGGATCATCACCCCATTTGTTACACACAC

-Gly 260 ||| TGGA 2219 uPro 280 ||||| ACCG 2279 ysar 304 ||||| AACG 2399 erTh 324 ||||| CAAC 2459 algl 344 ||||| TACA 2519 euGl 363 ||||| TGGG 2998 snTh 383 ||||| ||CAC 3058 TYFT 443 ||||| |AFT 3238 euAl 403 |||| |CGC 3118 Pher 423 |||| |TTA 3178 AAAA 2878 AAT 2818 AGT 2159 ACT 2339 AAA 2578 AAT 2638 CCC 2698 GCA 2758 356 TTC 2938 --- 356 --- 356 --- 356 356 --- 286 --- 356 956 ---

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1095 TITCCAGCICTCATITACTCCTCAATGGTGTGGG------TTGGTGAATATGGCA 1145
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                                                                                   615 GAGACTGTGGGCCAGAGGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTC 674
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                                            92 AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal
                                                                                                                                       112 ValValLeuMetThrValLeuLeuIleValPheTyrLysTyrLysPheTyrLysLeuIle
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                                              3239 ATATTAATTCTCTGTTTTTGCCATTTCTTTGCATCAACTTTTGGATTATATCT 3294
                        443 yrIleAsnSerLeuPheLeuProPheLeuCysIleIleAsnPheSerIleIleSer 461
                                                                                                                                                      Sequence 1, Application US/08706344C
Patent No. 624855
GENERAL INFORMATION:
APPLICANT: TANKI, RUDOLPH
APPLICANT: WASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial
TITLE OF INVENTION: Altheimer's Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERRE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,344C
FILING DATE: 30-AUG-1996
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INPORMATION:
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Matches:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity:
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US-08-706-344C-1
                                                                                                                                  US-08-706-344C-1
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             1617 ATGGACCAATTAGCATTCCAATTTAATATCTAGCATATTTGCGGTTAGAATCCATG 1676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 GlnGluAspGluAsnValValGluGluAlaGluLeuLysTyrGlyAlaSerHisValIle
                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
APPLICANT: WASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial
TITLE OF INVENTION: Alzheimer's Disease
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

RAPPLICATION NUMBER: US/08/706,344C
FILING DATE: 30-AUG-1996
CLASSIFICATION: 536
PRICA APPLICATION: 536
PRICA APPLICATION: 60/003,054
FILING DATE: 31-AUG-1995
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
APPLICATION NUMBER: 40,679
REGISTRATION NUMBER: 40,679
                                                                                                                                                                                                                                                           ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
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uHisLysSerLeuLysSerValTyrTyrIleAsnSerLeuPhe-
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Matches:
Conservative:
Mismatches:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                     Sequence 27, Application US/08706344C Patent No. 6248555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 061
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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994.50
65.17%
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TYPE: nucleic acid
STRANDEDNESS: double
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ADDRESSEE: STERNE, KA
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558 AGCTTTTATACCCGGAAGGATGGGCAG---CTAATCTATACCCCATTCACAGAAGATGC 614
                                                                                                                                                                                                                                                                            172 GlyAsnTyrGlyValLeuGlyMetMetCyslleHisTrpLysGlyProLeuArgLeuGln 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        915 CAGGCATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCT 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 GlufrpfhrValfrpPheValLeuPheValIleSerValfrpAspLeuValAlaValLeu 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                  192 GlnPheTyrLeuIleThrMetSerAlaLeuMetAlaLeuValPheIleLysTyrLeuPro 211
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ValValLeuMetThrValLeuLeuIleValPheTyrLysTyrLysPheTyrLysLeuIle 131
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                                                                         72 ThrPheTyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr 91
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440 GCAACAGCCAGTGGAGATTGGAACACAACACATAGCCTGTTTCGTAGCCATATTAATTGGT
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188 GAGACTGTGGGCCAGAGGCCCTGCACTCTGAATGCTGCCATCATGATCAGTGTC 247
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                                                                                                 132 HisGlyTrpLeuIleValSerSerPheLeuLeuLeuPheLeuPheThrThrIleTyrVal 151
                                                                                                                                                                                                                                                                                                                                        152 GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171
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 52 HißLeupheyalprovalSerLeuCysMetAlaLeuValValPheThrMetAsnThrlle 71
                                                                                                                                                                                                                          112 ValValLeuMetThrValLeuLeuIleValPheTyrLysTyrLysPheTyrLysLeuIle
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                                                                         72 ThrPheTyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr
                                                                                                                                                92 AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal
                                                                                                                                                                                                                                                                                                                                                                                                    368 GGGGAAGTGTTTAAAAACCTATAAAGGTTGTGTGTGGACTACATTACTGTTGCACTCCTGATC
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                         414 eProPheSerProAspSerPhePheThrPheValProAlaGlySerSerProHisLeuLe 434
                                                                         434 uHisLysSerLeuLysSerValTyrTyrIleAsnSerLeuPhe------LeuProPh 451
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IIILE OF INVENTION: ASSAY FOR IDENTIFYING GENES CAUSING
IIILE OF INVENTION: CHROMOSOME NON-DISJUNCTION
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216
77
104
48
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CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/08/875,972
FILING DATE: 08-AUG-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
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Matches:
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REIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,448
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Granahan Esq., Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: HU95-03PA
TELEPHONE: (731) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDUWITER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           Sequence 3, Application US/08875972
Patent No. 5985564
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: DNA (genomic)
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65.84%
48.54%
41.78%
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STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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Best Local Similarity: 48.54% Mismatches: 104 Query Match: 41.78% Indels: 48 DB: 9	US-09-043-944-1 (1-461) x US-08-923-454A-9 (1-2764) Qy 32 GlnGluAspGluAsnValGluGluAlaGluLeuLygTyrGlyAlaSerHisValIle 51	Db 438 GAGCAAGATGAGGAAGAAGAAGAGGTGACATTGAAATATGGCGCCAAGCATGTGATC 49	Qy 52 HisLeuPheValProValSerLeuCysMetAlaLeuValValPheThrMetAsnThrIle 71	72 ThrPheTyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr 9	Db 558 AGCTTTTATACCCGGAAGGATGGGCAGCTAATCTATACCCCATTCACAGAAGATACC 614	o [675 AITGIIGICAIGACHAICCICCIGGIGGITCIGIATAAAIACAGGIGCIAIAAGGICAIC	Qy 132 HisGlyTrpLeulleValSerSerPheLeuLeuLeuPheLbrhrThrIleTyrVal 151	Qy 152 GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171	Qy 172 GlyAsnTyrGlyValLeuGlyMetMetCysIleHisTrpLysGlyProLeuArgLeuGln 191	Db 855 1GGAATTTTGGTGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAG 91.	Qy 192 GlnPheTyrLeuileThrMetSerAlaLeuWalPheileLysTyrLeuPro 211	Qy 212 GlufrpThrValTrpPheValLeuPheVall1eSerValTrpAspLeuValAlaValLeu 231	2 5	252 PheProAlaLeulleTyrSerSerGlyVallleTyrProTyrValLeuValThrAlaVal	DB 1095 TTTCCAGCTCTCATTACTCCTCAACAATGGTGTGGTTGGTGAATATGGCA 114 Qy 272 GluAsHThrThrAspProArgGluProThrSerSerAspSerAspSerAspSerAshThrSerThrAlaPhe 291	Db 1146 GAAGGAGCCCGGAAGCTCAAAGGAGGTATCC11	Qy 292 ProGlyGluAlaSerCysSerSerGluThrProLysArgProLysValLysArgIlePro 311	Db 1188AAGTATAATGCAGAAAGCACAGAAAGG	312 GlnLysValGlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg	1215GAGTCACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAGT	Db 1260 GAGGAATGGGAAGGCCAGAGGACAGTCATCTAGGCCTCATCACGCTTACGCTCTACGCTTAGGTCA 131	
Qy 395 LeuCysPheThrLeuValLeuLeuAlaValPheLysArghlaLeuProAlaLeu-GlnPh 414	OY 414 eProPheSerProAspSerPhePheThrPheValProAlaGlySerSerProHisLeuLe 434	ProPh	Db 1190 ATGGACCAATTAGCATTCATCAATTTATATCTAGCATATTTGCGGTTAGAATCCCATG 1249 Ov 451 elemovellelle 455	1250 GATGTTCTTCTT	RESULT 5	US-US-323-4544-9; ; Sequence 9, Application US/08923454A; ; Patent No. 604794 . CENEDAL INDOMENTATION.	; GENERAL INFORMATION: APPLICANT: Cretha ; APPLICANT: Livi, George	Karra	20	<pre> CORRESPONDENCE ADDRESS: ADDRESSES: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia </pre>	; STATE: PA ; COUNTRY: USA ; ZIP: 19406	COMPUTER READABLE FORM: MEDIUM TYPE: Diskette	COMPUTER: IEM Compatible COMPUTER: IEM Compatible COPERATING SYSTEM: DOS COSTWARE: FastSEO Version 1.5	CORELL APPLICATION NUMBER: US/08/923,454A FILING DATE: CLASSIFICATION: 435	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 60/025436 ; FILING DATE: 06-SEPT-1996 ; ATTORNEY/AGENT INFORMATION:) NAME: Baumeister, Kirk ; REGISTRATION NUMBER: 33,833 ; REPERBUGE/DOCKER: P50547	; INLECTORIONS. TRYONOMING; TELEPHONE: 610-270-5096; TELEFAX: 610-270-5096	; INFORMATION FOR SEQ ID NO: 9: : SECHENCE CHARACTERISTICS:	LENGTH: 2764 base pairs	STRANDEDNESS: single	in H	ANTI-SENSE: NO FRAGMENT TYPE:	454P	Alignment Scores: 3.01e-104 Length: 2764 Score: 993.50 Matches: 216

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50 rcch---rchcctrrgggcrrgrifrcracrrrgcchcagarrarcrrgracagccfrff 1616
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Patent No. 6376239
GRIERAL INFORMATION:
APPLICANT: BAUMEISTER, Ralf
ITILE OF INVENTION: DNA MOLECULES COMPRISING A PROMOTER CAPABLE OF
ITILE OF INVENTION: CONFERRING EXPRESSION OF A HETEROLOGOUS DNA SEQUENCE IN
ITILE OF INVENTION: ALL NEURAL CELLS AT ALL STAGES OF DEVELOPMENT IN C.
ITILE OF INVENTION: ALL NEURAL CELLS AT ALL STAGES OF DEVELOPMENT IN C.
ITILE OF INVENTION: ALSO AND USES THEREOF
ITILE OF INVENTION: ALSO AND USES THEREOF
CURRENT APPLICATION NUMBER: US/08/832,867C
                                                    377 SerTyrPhe-----AspTrpAsnThrThrIleAlaCysTyrValAlalleLeulleGly 394
                                                                                                      LeuCysPheThrLeuValLeuLeuAlaValPheLysArgAlaLeuProAlaLeu-GlnPh 414
                                                                                                                                                       414 eProPheSerProAspSerPhePheThrPheValProAlaGlySerSerProHisLeuLe 434
                                                                                                                                                                                                            434 uHisLysSerLeuLysSerValTyrTyrIleAsnSerLeuPhe------LeuProPh 451
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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993.50
65.84%
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Best Local Similarity:
Query Match:
DB:
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US-08-832-867-2
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US-08-832-867-2
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1095 TTTCCAGCTCTCATTACTCCTCAACAATGGTGTGGG------TTGGTGAATATGGCA 1145
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                                                                                                                                                              794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheProAlaLeuIleTyrSerSerGlyValIleTyrProTyrValLeuValThrAlaVal 271
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675 ATTGITGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATC 734
                                                                                              132 HisGlyTrpLeulleValSerSerPheLeuLeuLeuPheLeuPheThrThrIleTyrVal 151
                                                                                                                                                                                                                           152 GlnGluValLeuLysSerFheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171
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                                                                                                                                       855 TGGAATTTTGGTGTGGTGGAATGATTTCCATTCACTGGAAAGTCCACTTCGACTCCAC
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975 GAATGGACTGCGTGGCTCATGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTG 1034
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                                                         92 AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal 111
                                                                              132 HisGlyTrpLeuIleValSerSerPheLeuLeuPheLeuPheLeuPheThrThrIleTyrVal 151
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                                                                                                                                                          TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK STREET: 600 SOUTH AVENUE WEST CITY, WESTFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHERING 3.0-017 CIP CIP IV
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Mismatches:
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                                                                                                                                     APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWNENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES
TITLE OF INVENTION: TO ALZHEIMER'S DIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,077A
FILING DATE: 03-UUL-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: 1..2675
OTHER INFORMATION: /note= "hPS1-1"
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APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                          Sequence 1, Application US/08888077A Patent No. 6020143 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNET THEORYATION
NAME: PALISI, THOMASALON
NAME: PALISI, THOMASALON
REGISTRATION NUMBER: 36,629
REPERENCE/DOCKET NUMBER: SCHER
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 654-7866
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 base pairs
TYPE: nucleic acid
STRANDENBESS: single
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993.50
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STATE: No COUNTRY: USA
TO 07090-1497
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Query Match:
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LOCATION: 249
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FEATURE:
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1440 GCAACAGCCAGTGGAACTGGAACACAACCATAGCCTGTTTCGTAGCCATATTAATTGGT 1499
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                                                         1560 TCCA --- TCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTACAGCCTTTT 1616
                                   434 uHisLysSerLeuLysSerValTyrTyrIleAsnSerLeuPhe------LeuProPh 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 GAGCAAGAIGAGGAAGAAGAIGAGGAGCTGACATTGAAATATGGCGCCCAAGCATGTGATC 497
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                                                                                                                                                                                                       US-08-967-101-133

Sequence 133, Application US/08967101

Patent No. 2840540

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWMENS, JOHANNA M
APPLICANT: RASER, PAUL E
APPLICANT: FRASER, PAUL E
APPLICANT: RASER, PAUL E
APPLICANT: FRASER, TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2791
216
77
104
48
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PCICASIFICATION DATA:
APPLICATION NUMBER: 08/592,541
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                B: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
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Matches:
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NAME: Pitcher, Edmund R.
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 2791 base pairs
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993.50
65.84%
48.54%
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                                                                                                             451 eLeuCysIleIle 455
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STATE: Massachusetts
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CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HUI
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ZIP: 02110
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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                                                                     172 GlyAsnTyrGlyValLeuGlyMetMetCyslleHisTrpLysGlyProLeuAxgLeuGln 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 GlnLysValGlnIleGluSerAsnThrThrAlaSerThrThrGlnAsnSerGlyValArg 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 SerTyrPhe-----AspTrpAsnThrThrIleAlaCysTyrValAlaIleLeuIleGly 394
92 AspSerIleValGluLySGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal 111
                                                                                                                                                132 HisGlyTrpLeulleValSerSerPheLeuLeuLeuPheLeuPheThrThrIleTyrVal 151
                                                                                                                                                                                                                                                                                                                                     855 TGGAATTTTGGTGTGGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAG 914
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                                                                                                                                                                                                                        152 GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171
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                   915 CAGGCATATCTCATTATGATTAGTCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCT
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1560 TCCA---TCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTACAGCCTTTT 1616
                                                     434 uHisLysSerVelLysSerValTyrIJeAsnSerLeuPhe------LeuProPh 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrPheTyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr
                                                                                                                                                                                                                                                                     APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWMENS, JOHANNA M
APPLICANT: ROWNENS, JOHANNA M
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2791
216
77
104
48
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-043-944-1 (1-461) x US-08-592-541-133 (1-2791)
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  Sequence 133, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: PICCHE, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR EQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 2791 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.06e-104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
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EDNESS: single
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CLASSIFICATION: 800
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                                                                                                                                                                                    RESULT 9
US-08-592-541-133
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DB:
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92 AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal 111
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CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
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High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                        APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: STOMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
ATTLE OF INVENTION: GENETIC SEQUENCES
TITLE OF INVENTION: TO ALZHEIMER'S DIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                    Sequence 133, Application US/09124698
Patent No. 6117978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Pitcher, Edmund R. TELECOMMUNICATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS;
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STATE: Massachusetts
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915 CAGGCATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTATCAAGTACCTCCCT 974
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                                                                                                         112 ValValLeuMetThrValLeuLeuIleValPheTyrLysTyrLy8PheTyrLySLeuIle 131
                                                                                                                                                                                                                                                       HisGlyTrpLeuIleValSerSerPheLeuLeuLeuPheLeuPheThrThrIleTyrVal 151
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216
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104
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-043-944-1 (1-461) x US-09-127-480-133 (1-2791)
                                                                                                        Sequence 133, Application US/09127480
Patent No. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PRO;
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
ILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:
PLILOR PICCHE, Edmund R.
TELEPHONE: (617) 248-7000
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER/STICS:
SEQUENCE CHARACTER/STICS:
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                                                            1677 GATGITICITI 1689
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TYPE: nucleic acid
STRANDEDNESS: single
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65.84%
48.54%
                                      451 eLeuCysileile 455
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                                                                                                                                                                                                                                                                                                    02110
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                       RESULT 11
US-09-127-480-133
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975 GAAIGGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTG 1034
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                                                                                                                                                                                                                                                                                                                                                      172 GlyasnTyrGlyValLeuGlyMetMetCyslleHisTrpLysGlyProLeuArgLeuGln 191
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                                               132 HisGlyTrpLeuIleValSerSerPheLeuLeuLeuPheLeuPheThrThrIleTyrVal 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 GInGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171
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AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal 111
                                                                                                                                                   112 ValValLeuMetThrValLeuLeuIleValPheTyrLysTyrLysPheTyrLysLeuIle 131
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                                                                                                                                                                                                                                                                                                                                                APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWENS, JOHANNA M
APPLICANT: RASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2791
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77
104
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Mismatches:
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STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/124,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            Sequence 133, Application US/09124523
Patent No. 6395960
GENERAL INFORMATION:
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NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 133:
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LENGTH: 2791 base pairs
TYPE: nucleic acid
                                                                                       451 eLeuCysileile 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            993.50
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1146 GAAGGAGACCCGGAAGCTCAAAGGAGTATCCAAAATTCC------- 1187
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                                             172 GlyabnTyrGlyValLeuGlyMetMetCysIleHisTrpLysGlyProLeuArgLeuGln 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phe ProAlaLeuIleTyrSerSerGlyValIleTyrProTyrValLeuValThrAlaVal 271
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92 AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal 111
                                                                                                                                            112 ValValLeuMetThrValLeuLeuIleValPheTyrLysTyrLysPheTyrLysLeuIle 131
                                                                                                                                                                                                                                                                                    HisGlyTrpLeulleValSerSerPheLeuLeuLeuPheLeuPheThrThrIleTyrVal 151
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1035 TGTCCGAAAGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAATGAAACTT 1094
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TIGIGCCTIACATIATIACICCTIGCCATITICAAGAAAGCAIIGCCAGCICTICCAAIC 1559
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                                                                                                                             HisGlyTrpLeulleValSerSerPheLeuLeuLeuPheLeuPheThrThrIleTyrVal 151
                                                                                                                                                                                      GlnGluValLeuLysSerPheAspValSerProSerAlaLeuLeuValLeuPheGlyLeu 171
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                                      GlnPheTyrLeuIleThrMetSerAlaLeuWetAlaLeuValPheIleLysTyrLeuPro
                                                                         ValValLeuMetThrValLeuLeuIleValPheTyrLysTyrLysPheTyrLysLeuIle
                    AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 HisLeuPheValProValSerLeuCysMetAlaLeuValValPheThrMetAsnThrIle 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrPheTyrSerGlnAsnAsnGlyArgHisLeuLeuSerHisProPheValArgGluThr 91
                                                                                                                                                                                                           TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                   COUNTY: U.S.A.

ZIP: 0210

ZIP: 0210

COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: DESTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

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ATTORNEY/AGENT INFORMATION:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                  ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: High Street Tower - 125 High
                                                                                                                                                                   APPLICANT: ST. GEORGE-HYSLOP, PETER H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO: 133:
                                                                                                                       Sequence 133, Application US/09636796A Patent No. 6485911 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (617) 248-7000
                                                                                                                                                                              ROMMENS, JOHANNA M
FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2791 base pairs
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INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
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65.84%
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CORRESPONDENCE ADDRESS:
                                                             1677 GATGTTTCTTT 1689
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                                                                                             RESULT 13
US-09-636-796A-133
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                                                                           112 ValValLeuMetThrValLeuLeulevalPheTyrLysTyrLysPheTyrLysLeulle 131
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                                                                                                                                                          132 HisGlyTrpLeulleValSerSerPheLeuLeuPheLeuPheLeuPheThrThr1leTyrVal 151
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                      615 GAGACTGTGGGGCCGGAGGCCCTGCACTCTGAATGCTGCCGCCATCATGTGGTGTC
                                                                                               855 TGGAATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAG
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92 AspSerIleValGluLysGlyLeuMetSerLeuGlyAsnAlaLeuValMetLeuCysVal
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                                                                                                                                                                                                                                                                                         FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: <UNKNOWn>
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Matches:
Conservative:
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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 133:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
                                                                                                                                                                                           Sequence 133, Application US/08496841C
Patent No. 6210919
GENERAL INFORMATION
APPLICANT: ST. GEORGE-HYSLOP, PF
ROYMENS, JOHANNA M
FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 753-6237 INFORMATION FOR SEQ ID NO: 133: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2792 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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993.50
65.84%
48.54%
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                                                                                                    1677 GATGTTTCTTCTT 1689
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COMPUTER READABLE FORM:
                                                                             451 eLeuCysileile 455
                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: U.S.A.
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                                                                                                                                                        RESULT 14
US-08-496-841C-133
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215
72
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Patent No. 6010874

GENERAL INFORMATION:
APPLICANT HARDY, John A.
ITLE OF INVENTION: GENE AND GENE PRODUCTS

TITLE OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTR::
2IP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: EMASTER DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATE: 26-JUN-1996
FILING DATE: 26-JUN-1996
FILING DATE: 26-JUN-1996
FILING DATE: 26-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Secondary Secondary Corporation 709 Swedeland Road - UW2220; P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,142
FILING DATE: 13-JUL-1995
APPLICATION NUMBER: 60/001,501
FILING DATE: 18-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: HAIN, WILliam T
REGISTRATION NUMBER: 34,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 34,344
REFERENCE/DOCKET NUMBER: P50358
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TRIBEROY.
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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65.98%
49.43%
41.67%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Philadelphia
STATE: PA
COUNTRY: USA
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Best Local Similarity:
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US-08-670-964-3
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Query Match:
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Search completed: December 11, 2003, 07:43:07 Job time : 122 secs